



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122411

TO: Karen A Lacourciere
Location: REM-2D15/2C18
Art Unit: 1635
May 24, 2004

Case Serial Number: 09/301380

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 20:13:21 ; Search time 1486 Seconds
(without alignments)
11818.338 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 ctcaagaatccccgcacga.....tggtagagagatattttc 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
5: geneseqn20018:*
6: geneseqn20028:*
7: geneseqn20038:*
8: geneseqn20038:*
9: geneseqn20038:*
10: geneseqn20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4134	100.0	4134	3	AAZ38152 Human Nr-
2	3751.6	90.7	3997	2	AAV62739 Human neu
3	3316	80.2	6253	3	AAV64155 Nucleotid
4	3316	80.2	6254	2	AAV40887 Coding se
5	3316	80.2	6254	5	AAFP8452 Human CDN
6	3233.6	78.2	6384	10	ADE77114 Human CDN
7	2226	54.1	3943	6	AA516294 CDNA enco
8	1371	33.2	1371	3	AAZ38181 Human Nr-
9	1092.6	26.4	1371	3	AAZ38182 Rat Nr-CA
10	779.8	18.9	4360	7	AAAD9596 Human cyt
11	778.2	18.8	4080	7	AAAD9595 Human cyt
12	737.2	17.0	4131	7	ABT16046 NOVX rela
13	702.4	17.0	4739	4	AAK51848 Human pol
14	676.6	16.4	4694	4	AAK51847 Human pol
15	445.4	10.8	2462	9	ADBE1924 Human CDN
16	405.8	9.8	3783	6	AA516288 CDNA enco
17	405.4	9.8	5093	3	ADBS2876 Primary r
18	379	9.2	7722	5	AA585546 DNA enco
19	358.6	8.7	416	2	AAV87228 EST clone
20	351	8.5	3774	2	AAK01588 Human LI
21	347	8.4	3888	6	AA516282 CDNA enco
22	340	8.2	445	4	AB457607 Human foe
23	340	8.2	445	4	AA137168 Probe #58

C 24	340	8.2	445	4	AAK31269	AAK31269 Human bon
C 25	340	8.2	445	4	AAK05659	AAK05659 Human bra
C 26	340	8.2	445	4	ABS30949	ABS30949 Human liv
C 27	340	8.2	445	6	ABS06021	ABS06021 Human gen
C 28	340	8.2	3250	4	AA105627	AA105627 Human rep
C 29	284.4	6.9	694	6	ABT09020	ABT09020 Phase-1 R
C 30	231.8	5.6	32176	4	AA105628	AA105628 Human rep
C 31	231	5.6	469	4	AA58940	AA58940 Human foe
C 32	231	5.6	469	4	AA138658	AA138658 Probe #73
C 33	231	5.6	469	4	AAK32843	AAK32843 Human bon
C 34	231	5.6	469	4	AAK07103	AAK07103 Human bra
C 35	231	5.6	469	4	ABS32568	ABS32568 Human liv
C 36	231	5.6	469	6	ABS07647	ABS07647 Human gen
C 37	230	5.6	230	4	ABA70229	ABA70229 Human foe
C 38	230	5.6	230	4	AA150358	AA150358 Probe #19
C 39	230	5.6	230	4	AAK44359	AAK44359 Human bon
C 40	230	5.6	230	4	AAK18454	AAK18454 Human bra
C 41	230	5.6	230	4	ABS44016	ABS44016 Human liv
C 42	230	5.6	230	6	ABS18595	ABS18595 Human gen
C 43	224	5.4	224	4	ABA71469	ABA71469 Human foe
C 44	224	5.4	224	4	AA151738	AA151738 Probe #20
C 45	224	5.4	224	4	AAK45811	AAK45811 Human bon

ALIGNMENTS

RESULT 1	AAZ38152	standard; DNA; 4134 BP.
ID	AAZ38152	
XX	AAZ38152;	
AC	14-FEB-2000	(first entry)
XX		
DT	Human Nr-CAM gene sequence.	
XX		
DE		
XX		
KW	Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation;	
KW	tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;	
KW	degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;	
KW	systemic lupus erythematosus; demyelinating disease; growth; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9955380-A1.	
XX		
PD	04-NOV-1999.	
XX		
PF	27-APR-1999;	99WO-US009039.
XX		
PR	27-APR-1998;	98US-0083152P.
PR	14-DEC-1998;	98US-0112098P.
XX		
PA	(PACI-) PACIFIC NORTHWEST CANCER FOUND.	
PI	Murphy GP, Boynton AL, Sehgal A;	
XX		
XX	WPI; 2000-023268/02.	
DR	P-PSDB; AAY40439.	
XX		
PT	Use of neuron-glia-related cell adhesion molecule for developing agents	
PT	for the diagnosis and treatment of e.g. cancers, hyperproliferative	
PT	disorders, growth deficiencies, degenerative disorders, trauma or wounds.	
XX		
PS	Disclosure; Page 165-171; 183pp; English.	
XX		
CC	The invention relates to the use of neuron-glia-related cell adhesion	
CC	molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or	
CC	preventing disorders involving cell proliferation. An antisense nucleic	
CC	acid complementary to at least a portion of an RNA transcript of a Nr-CAM	
CC	gene can be used to inhibit hyperproliferation of a tumor cell, for the	
CC	treatment of tumorigenesis. Agents which inhibit Nr-CAM function can be	
CC	used to treat or prevent malignancies, e.g. brain cancer, leukemia, B	

cell lymphoma, premalignant conditions, benign tumors, hyperproliferative
disorders or benign dysproliferative disorders. Such treatment is
especially useful for treating glioblastoma, glioma, meningioma,
astrocytoma, medulloblastoma, neuroectodermal cancer and neuroblastoma,
especially glioblastoma multiforme. Agents which promote Nr-CAM function
may also be used to treat or prevent degenerative disorders, growth
deficiencies, hypoproliferative disorders, physical trauma, lesions or
wounds. In particular, they can be used for treating e.g. traumatic,
ischemic, malignant and degenerative lesions and alcoholic cerebellar
degeneration. Also described is the treatment of lesions associated with
systemic diseases e.g. diabetes or systemic lupus erythematosus, lesions
caused by toxic substances e.g. alcohol, lead or other toxins; and
demyelinated lesions of the nervous system, in which a portion of the
nervous system is destroyed or injured by a demyelinating disease e.g.
multiple sclerosis, HIV-associated myelopathy, transverse myelopathy of
various etiologies, progressive multifocal leukoencephalopathy or central
pontine myelinolysis; or lesions of the central or peripheral nervous
systems. In addition, agents which promote Nr-CAM function can be
promoted to increase growth of animals (e.g. cows, horses, pigs, goats,
deer, chickens) and plants (particularly edible plants, e.g. tomatoes,
melons, lettuce, carrots, potatoes, and other vegetables), particularly
those that are food or material sources. They can also be used in vitro
e.g. to expand cells e.g. stem cells, progenitor cells, muscle cells,
fibroblasts, or liver cells to grow cells/tissue in vitro prior to
administration to a patient. The products can also be used for detection,
diagnosis and production of animal models. The present sequence
represents the nucleotide sequence of the human Nr-CAM gene

XX Sequence 4134 BP; 1256 A; 904 C; 955 G; 1019 T; 0 U; 0 Other;

Query Match 100.0%; Score 4134; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTTCAAGTCCCGCATGAATTAATTCTTAACGTTGACACACAGCTTTCAGAAATCTT 60
1 CTTCAAGTCCCGCATGAATTAATTCTTAACGTTGACACACAGCTTTCAGAAATCTT 60
61 TTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
61 TTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
121 CTTAAATATATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
121 CTTAAATATATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
181 CTGTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
181 CTGTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
241 GTACAGCTCCCAACATCAACCAAGCTTCGAAAGATTACATTTTGAAGCTTGGAG 300
241 GTACAGCTCCCAACATCAACCAAGCTTCGAAAGATTACATTTTGAAGCTTGGAG 300
301 AATATTTGATCCAGTGTGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
301 AATATTTGATCCAGTGTGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
361 AATGGAATCTATTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 420
361 AATGGAATCTATTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 420
421 AATGGAATCTATTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 480
421 AATGGAATCTATTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 480
481 TGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
481 TGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
541 AGATCAACATTTGTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 600
541 AGATCAACATTTGTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 600

601 TTAGACTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
601 TTAGACTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
661 AATTCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
661 AATTCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
721 TATTTTCCAAATGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
721 TATTTTCCAAATGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
781 AATCACTCAACCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 AATCACTCAACCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 GAATTAATGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 GAATTAATGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
901 AGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 AGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
961 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
961 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
1021 TACTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1021 TACTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1081 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1081 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1141 AAAAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1141 AAAAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
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1381 CAAGAAAGATCAAGTATATGATGATGATGATGATGATGATGATGATGATGATG 1440
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1441 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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1741 ATGGCAAAAGATTAAGTCTTACAGCCCGAATATGCAAGTTGTGCAAAAGAGGACAG 1800
1741 ATGGCAAAAGATTAAGTCTTACAGCCCGAATATGCAAGTTGTGCAAAAGAGGACAG 1800
1801 GTGTCTTTGAATGCAAGTGAAGACATGATCAACCTTATCCCTCACTGTGCTGTGGCTG 1860
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1861 AAGGACAAAGAGGACCTGCGCAGTGAAGAGTTGCACTGTTGACAGAGTCACTAGTG 1920
1861 AAGGACAAAGAGGACCTGCGCAGTGAAGAGTTGCACTGTTGACAGAGTCACTAGTG 1920
1921 GTTGTGATGTGTCAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
1921 GTTGTGATGTGTCAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
1981 GACAGGCTCTCCGCGCAGGCTGTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2040
1981 GACAGGCTCTCCGCGCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2040
2041 GTTTAGATGTGTCAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
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2101 GTTGTGATGTGTCAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
2161 GAATATGAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
2161 GAATATGAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
2221 AACACAGACCAAGCCAGCTGAGTGTCTCTTGTGAGTGAAGTGAAGTGAAGTGAAGTGA 2280
2221 AACACAGACCAAGCCAGCTGAGTGTCTCTTGTGAGTGAAGTGAAGTGAAGTGAAGTGA 2280
2281 GAGTGAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
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2341 GCTTGAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
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2401 TTGAGATTAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2460
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2461 AAGGTTAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
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2521 GATATGAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
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2581 GGCCTGAATGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
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2761 ATTACTATTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
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2941 AAGGTTGAATTAATCTCAGAGAGGAGTCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 3000
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3181 GATTTGAATTAATCTCAGAGAGGAGTCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 3240
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3241 GAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3300
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3361 AATATCAGTGTGAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
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3421 GAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
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3421 GAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
3481 TTTAAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
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3541 GGTTTGTGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
3541 GGTTTGTGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
3601 GATATGAAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3660
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3661 ATTTGTGATTAATCTCAGAGAGGAGTCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 3720
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3721 AAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
3721 AAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
3781 GAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3840
3781 GAGGAGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3840
3841 GACAGAGTGTGAAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3900

Db 3841 GACAGACTGTGTAAGAAAAAGATAGTACAGACAGCTAGTACTATGAGAGAGGGCTT 3900
Qy 3901 AATGGCAATTTAAATAGATGCTCTTATTTGACATATGAGTGTAAAGAGAA 3960
Db 3901 AATGGCAATTTAAATAGATGCTCTTATTTGACATATGAGTGTAAAGAGAA 3960
Qy 3961 GAGCCGCTGAAAGAAAGAGCTCAGAGGACCTTCTCTCAACCCATGATTC 4020
Db 3961 GAGCCGCTGAAAGAAAGAGCTCAGAGGACCTTCTCTCAACCCATGATTC 4020
Qy 4021 TTTGTTTAAATTTTAAAGCTCAAGCAATATTCATTTCTCTGAAATGTTTATCTTAAAC 4080
Db 4021 TTTGTTTAAATTTTAAAGCTCAAGCAATATTCATTTCTCTGAAATGTTTATCTTAAAC 4080
Qy 4081 TCTGTTTGTGAGCCCTCTCATATCTATGAAATATGAGTGTAAAGAGTATTTTC 4134
Db 4081 TCTGTTTGTGAGCCCTCTCATATCTATGAAATATGAGTGTAAAGAGTATTTTC 4134

RESULT 2
AAV62739
ID AAV62739 standard; cDNA; 3997 BP.
XX AAV62739;
AC
XX
DT 02-FEB-1999 (first entry)
XX
DE Human neural cell adhesion molecule NRCAMvar cDNA.
XX
KW NRCAMvar; NRCAM; neural cell adhesion molecule; human; diabetes; obesity;
KW cancer; therapy; diagnosis; vaccine; ss.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT 18..3932
FT CDS /*tag= a
FT
XX
PN MO9836062-A1.
XX
PD 20-AUG-1998.
XX
PF 12-FEB-1998; 98WO-GB000434.
XX
PR 13-FEB-1997; 97GB-00003011.
PR 22-JUL-1997; 97EB-00305485.
XX
PA (SMK) SMITHKLINE BEECHAM PLC.
XX
PI Terrett JA, Kenwick SJ, Wang B;
XX
DR MPI, 1998-520757/44.
XX
DR P-PDB; AAM59994.
XX
PT NRCAM-related cell adhesion molecule splice variant polypeptide NRCAMvar
PS - used to treat diabetes, obesity and cancer.
XX
PS Claim 4; Page 20-22; 32pp; English.
XX
CC This is the nucleotide sequence of a cDNA clone encoding a splice
CC variant, designated NRCAMvar (see AAM59994), of human neural cell
CC adhesion molecule NRCAM. The HGS EST database was screened using the
CC chick NRCAM sequence, and 3 EST clones were obtained from human adrenal
CC and striatum cDNA libraries. Fragments homologous to NRCAM were end-
CC sequenced and used as probes to screen a human foetal brain cDNA library.
CC 4 Positive clones were isolated and inserts were subcloned into
CC pBluescript plasmids. Additional sections of the gene were isolated using
CC gene-specific primers to amplify cDNA from human foetal brain libraries.
CC The DNA sequence of human NRCAMvar is 77.1% identical to that of the
CC chick gene. NRCAMvar polypeptides and polynucleotides are methods of
CC producing such polypeptides by recombinant techniques and disclosed. Also
CC disclosed are methods for utilising such polypeptides and polynucleotides
CC in the design of protocols for the treatment of conditions associated

CC with NRCAM imbalance, including diabetes, obesity and cancer, as well in
CC diagnostic assays for such conditions, and in vaccines. The nucleotide
CC sequence can be used to diagnose diseases caused by a mutation of the
CC NRCAMvar polypeptide or to screen a library for NRCAMvar homologues
XX
SQ Sequence 3997 BP; 1203 A; 888 C; 928 G; 978 T; 0 U; 0 Other;
Query Match 90.7%; Score 3751.6; DB 2; Length 3997;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3867; Conservative 0; Mismatches 59; Indels 60; Gaps 2;
Qy 103 GGAATTAAGCTATATGACCTTAAATTAATGCGGAAAAAGAGCCCTTATCTGCGGGCGA 162
Db 6 GGAATTAAGCTATATGACCTTAAATTAATGCGGAAAAAGAGCCCTTATCTGCGGGCGA 65
Qy 163 GTGCCCCGATTTCTCTCTGCGAGATGATAGTGTGACCTGAGTACCTTATGATCA 222
Db 66 GTGCCCCGATTTCTCTCTGCGAGATGATAGTGTGACCTGAGTACCTTATGATCA 125
Qy 223 AAATCTTGTGAAGACTGTGACAGCTCCAAACCATCAACCAACAGCTCTCAAAAGATTAC 282
Db 126 AAATCTTGTGAAGACTGTGACAGCTCCAAACCATCAACCAACAGCTCTCAAAAGATTAC 185
Qy 283 ATTATTTGACCTCGGAGAAATTTGTATTCAGTGTGAAGCCAAAGGAAACCGCCCCA 342
Db 186 ATTATTTGACCTCGGAGAAATTTGTATTCAGTGTGAAGCCAAAGGAAACCGCCCCA 245
Qy 343 AGCTTTCTGACCCCGTAATGAGGACATGTTTGAATGATGAAAGCCCTGCTGAC 402
Db 246 AGCTTTCTGACCCCGTAATGAGGACATGTTTGAATGATGAAAGCCCTGCTGAC 305
Qy 403 ATGAAGCCGTGACAGAAAGCTCATTAATTAATCATATGAGGAAAGGAAAGCTGAGAC 462
Db 306 ATGAAGCCGTGACAGAAAGCTCATTAATTAATCATATGAGGAAAGGAAAGCTGAGAC 365
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Db 546 ATTAATTTTGGATGATTAATCTTTTCAAGACTTCCAAAGTGAAGAGATTCTCA 605
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Db 606 GGTGTTGATGAGGAGCTTATTTTCAATGCTCCAGAGAGACCCGAGAGACTAT 665
Qy 763 ATCTGTTATGCTAGATTTATATCATCTCAACCATACAGAGAAACCTTATCTG 822
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Db 1596 GCAAGGAATTAATTAGGATGCGAAAGATGAAGTTCACTTAGAAATCAAAAGTCTTACA 1655
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Qy 1993 GCGAGGCTGTGCTTACGCTGTGCTCACTCAACTCAGACTCCGTTTACAGATGTC 2052
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Db 2136 GCGCAGCTGAAGCTGTCTTACGTGAATCTACTCTTCCGCTGATGAGAGTGAACAGC 2195
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Db 2196 AATTGGAAAGCTTCCAGAGGAGCTGTGAGAGTATTTGACGAAGAGCTCAGAACCA 2255
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Db 2616 GACCCAGTACCTCTGAAAAGCATCCGAGAGCACTTACAGAGCTATCGAATTTACTATTGG 2675
Qy 2773 AAGACCCAGAGTTCACTTAAAGAAACAGAGCTCACTTGAAGAAAGATCTTCACTTC 2832
Db 2676 AAGACCCAGAGTTCACTTAAAGAAACAGAGCTCACTTGAAGAAAGATCTTCACTTC 2735
Qy 2833 CAAGGACAGAGCTCATGAGCATGTGCGGAGGCTAGAGCCCTTGAAGCACTACACCTG 2892
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Db 3456 TCAGAGATGTGTGTGAGACAGGCGCAGAGATGAGCAAGCCGAGAGTGAATATGCAACT 3515
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QY 4033 TTAAGCTCAAGGCAATATTCATTT 4058
Db 3936 TAGAAGCTTGAATTCGATGATGCTTT 3961

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KW osteoporosis; osteoarthritis; periodontal disease; tooth repair;
KW nervous system disorder; angiogenic activity; fibrosis; fertility;
KW reperfusion injury; systemic cytokine damage; contraceptive;
KW thrombolytic; coagulation disorder; antiinflammatory activity;
KW inflammatory condition; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 383..3961
FT /tag= a
FT /product= "secreted protein"
PD WO20050592-A1.
PD 31-AUG-2000.
PF 24-FEB-2000; 2000WO-US004731.
PR 24-FEB-1999; 99US-00256938.
PA (GENV) GENETICS INST INC.
PI Jacobs K, McCoy JM, Lavalie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR, Spaulding V;
DR MPI: 2000-558399/51.
DR P-P8DB; AAB08442.
PT New secreted polypeptides and nucleic acids encoding them used for
PT treating various anemias, bone, cartilage, tendon, ligament and/or nerve
PT tissue or regeneration, contraceptives, and nutritional supplements.
BS Disclosure: Page 104-105; 119pp; English.
XX The present sequence encodes a human secreted protein. The polypeptides
XX may be used in the treatment of various immune deficiencies and
XX disorders, and to treat infectious diseases caused by viral, bacterial,
XX fungal or other infections. The polypeptides are also used in
XX compositions for bone, cartilage, tendon, ligament and/or nerve tissue
XX growth or regeneration, for wound healing and tissue repair and
XX replacement, and in the treatment of burns, incisions and ulcers. The
XX protein is used in the treatment of osteoporosis or osteoarthritis,
XX periodontal disease and other tooth repair processes, and nervous system
XX disorders. They also exhibit angiogenic activity and protect, regenerate
XX and treat lung or liver fibrosis, reperfusion injury in various tissues,
XX and conditions resulting from systemic cytokine damage. They promote or
XX inhibit tissue differentiation and are used as contraceptives and to
XX enhance fertility. They also have a hemostatic or thrombolytic activity
XX and can be used to treat various coagulation disorders. They also have an
XX antiinflammatory activity and can be used to treat inflammatory
XX conditions
SQ Sequence 6253 BP; 1978 A; 1274 C; 1292 G; 1704 T; 0 U; 5 Other;
XX
XX
Query Match 80.2%; Score 3316; DB 3; Length 6253;
Best local Similarity 90.2%; Pred. NO. 0;
Matches 3758; Conservative 0; Mismatches 10; Indels 396; Gaps 4;
QY 1 CTTCAAAGTCCCGCATGAAAATTACTTAAACGTGACACACAGCTTTCAGAAAATCTT 60
Db 269 CTTCAAAGTCCCGCATGAAAATTACTTAAACGTGACACACAGCTTTCAGAAAATCTT 328
QY 61 TTGTGAAAAGAAAAGAAAATTCTGCTGTGAGCTCAGACAGAGTTAACTAATGAG 120
Db 329 TTGTGAAAAGAAAAGAAAATTCTGCTGTGAGCTCAGACAGAGTTAACTAATGAG 388
QY 121 CTTAAATATATCCGAAAAGAGAGCGCTTATCTGTGGGCAAGAGTCCCTGATCTCTTC 180
Db 389 CTTAAATATATCCGAAAAGAGAGCGCTTATCTGTGGGCAAGAGTCCCTGATCTCTTC 448
QY 181 CTGTCCAGATGATTAGTGCAGTGGAGTACTCTTGATCCAAAACCTTGAAGACTTG 240

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RESULT 3
AAA64155
ID AAA64155 standard; cDNA; 6253 BP.
XX
XX AAA64155;
XX
XX
XX 20-DEC-2000 (first entry)
DE Nucleotide sequence of secreted protein clone C0722_1.
XX
XX Human; secreted protein; immune deficiency; infectious disease;
KW tissue growth; wound healing; tissue repair; burn; incision; ulcer;

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Db 449 CTGTCCAGATGATTAGTGAAGTGAAGTCTCTTGAATCCAAACTTCTTGAAGACTTGG 508
 Qy 241 GTACAGCCTCCAAACATCAACCAAGCTCTCCAAAGATTATTAATTTGACCTCGGAG 300
 Db 509 GTACAGCCTCCAAACATCAACCAAGCTCTCCAAAGATTATTAATTTGACCTCGGAG 568
 Qy 301 AATATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTTGAAGCTCGT 360
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 Qy 361 AATGGACATCTTTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 420
 Db 629 AATGGACATCTTTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 688
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 Db 689 ACGCTCATATTATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 748
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 Db 749 TGTACAGAGAAAGCAAGCGGAGCTGCAATTTCTAATCAATTTGTGTCCGCTCATC 808
 Qy 541 AGATCCATCTTTGAGCAAGAAAGAACTTTGAACATCACTTCAAGTGTCTCATCT 600
 Db 809 AGATCCATCTTTGAGCAAGAAAGAACTTTGAACATCACTTCAAGTGTCTCATCT 868
 Qy 601 TTATGATCTCCCTGAGACCCCAATTTGATTAACCACTAATTAATTTTGAAGTAT 660
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 Qy 1621 GTTTTACATGAAATGGAATCTTTGGAATCAAGATGCTACATGATGTTAAAGAAAT 1680
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 Qy 1681 CCTGTGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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 Db 1922 ATGGCAAGAGATGAAGTCACTTAAAGATGAGTCAATGAGTGTAAACAGCC 1981
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 QY 2851 GGCATTTGCCGGGGCTAGAGCCCTTTAGCCACTACACATGATTTCCGAGTGTCAAT 2910
 DB 3062 GGCATTTGCCGGGGCTAGAGCCCTTTAGCCACTACACATGATTTCCGAGTGTCAAT 3121
 QY 2911 GGGAAAGGGGAGGGCCCAAGCAGCCCTGATTAATTAATCTCAGAAAGAGTCCCC 2970
 DB 3122 GGGAAAGGGGAGGGCCCAAGCAGCCCTGATTAATTAATCTCAGAAAGAGTCCCC 3181
 QY 2971 AGTGTCTCCCTCGCTTTGGAAGATTTGGAATCCAACTGGAATCTCTCACTTTGGAATGG 3030
 DB 3182 AGTGTCTCCCTCGCTTTGGAAGATTTGGAATCCAACTGGAATCTCTCACTTTGGAATGG 3241
 QY 3031 GATCCACGAGCCACCCGGAATGGCATTTTGAAGAGTACACCTTAAGTATGAGCCAAAT 3090
 DB 3242 GATCCACGAGCCACCCGGAATGGCATTTTGAAGAGTACACCTTAAGTATGAGCCAAAT 3301
 QY 3091 AACAGACACATGAATTAAGCCCTCTGTGATTTGAAATTCCTGCCAACAAGACACGG 3150
 DB 3302 AACAGACACATGAATTAAGCCCTCTGTGATTTGAAATTCCTGCCAACAAGACACGG 3361
 QY 3151 TGGACTTTTAAAAAATTTAAATTTGAGACATCGATTAATGATTTTCTATGCAAAACA 3210
 DB 3362 TGGACTTTTAAAAAATTTAAATTTGAGACATCGATTAATGATTTTCTATGCAAAACA 3421
 QY 3211 TCAGCAGATCAGGAAGTCAAAATTAACAGAGAGAGTAAACAACCTGTGATGAAGCTGGT 3270
 DB 3422 TCAGCAGATCAGGAAGTCAAAATTAACAGAGAGAGTAAACAACCTGTGATGAAGCTGGT 3481
 QY 3271 ATTCTTCCACCTGATGATGGTGAAGCAAGTTCAAGCTGTAAATACAGAGATCAGCAAT 3330
 DB 3482 ATTCTTCCACCTGATGATGGTGAAGCAAGTTCAAGCTGTAAATACAGAGATCAGCAAT 3510
 QY 3331 CTTAAGCTGACAGCTGTGAGACCTATGCAATATCAGTTGGGAATATGAGGACCAAG 3390
 DB 3511 ----- 3510
 QY 3391 CATGTGAATTTATGTTGAATATGGGTAGCAGGACAGAAAGATGAGAAAGAA 3450
 DB 3511 ----- 3510
 QY 3451 ATTGTAATGGTTCTCGAGCTTCTTTGGTTAAAGGCTTAATGCCAGAAACAGCATAC 3510

DB 3511 ----- 3510
 QY 3511 AAAGTTGAGTTGGTCTGTGGGGGACTGTGGTTTGTGAGTTGAGAGATGTTGAG 3570
 DB 3511 ----- 3510
 QY 3571 ACAGGCCAGGATGAGGACCGGAGGTGATTAATGCACTCAGGCTGTTCATGCT 3630
 DB 3511 ----- AGCATGCGAAGCCGGCAGGTGATTAATGCACTCAGGCTGTTCATGCT 3562
 QY 3631 CTGATGTGTGCTGTGCTCTCTCTTATTTTAAATTTTGTGATTTGCTTATGCAAGA 3690
 DB 3562 CTGATGTGTGCTGTGCTCTCTCTTATTTTAAATTTTGTGATTTGCTTATGCAAGA 3622
 QY 3691 AACAGGGGTGTAATATCCAGTTAAAGAAAGAAAGATGCCATGCTGACCTGAAATC 3750
 DB 3622 AACAGGGGTGTAATATCCAGTTAAAGAAAGAAAGATGCCATGCTGACCTGAAATC 3682
 QY 3751 CAGCCTATGAAGAGATGATGAGCATTTGGAGATACAGTATGACAGAAACCAAG 3810
 DB 3683 CAGCCTATGAAGAGATGATGAGCATTTGGAGATACAGTATGACAGAAACCAAG 3742
 QY 3811 CTTTGAAGAAAGAAAGTGCATCTCTTCAACAGAGATCTGGAAGAAAGAAATGATGAC 3870
 DB 3743 CTTTGAAGAAAGAAAGTGCATCTCTTCAACAGAGATCTGGAAGAAAGAAATGATGAC 3802
 QY 3871 GACAGCTAGTTGACTATGAGAAAGGGTTAATGSCAGTTCAATGAGATGCTCTTT 3930
 DB 3803 GACAGCTAGTTGACTATGAGAAAGGGTTAATGSCAGTTCAATGAGATGCTCTTT 3862
 QY 3931 ATTGCAATATCAGTGTGAAGAAAGAAAGAGCCGCTGAAGAAAGAAAGTCTCAG 3990
 DB 3863 ATTGCAATATCAGTGTGAAGAAAGAAAGAGCCGCTGAAGAAAGAAAGTCTCAG 3922
 QY 3991 GACCTTCTCCCTGTGAAGCCCATGAAATCTTTGTTAATTTTAAAGCTTCAAGCCAA 4050
 DB 3922 GACCTTCTCCCTGTGAAGCCCATGAAATCTTTGTTAATTTTAAAGCTTCAAGCCAA 3982
 QY 4051 TTGCAATTTCTAGAAGTTTATCTTAAGCTCTTGTGTGAGCCCTCATATGATGA 4110
 DB 3983 TTGCAATTTCTAGAAGTTTATCTTAAGCTCTTGTGTGAGCCCTCATATGATGA 4042
 QY 4111 CATATGGGTAGAGATATATTTTC 4134
 DB 4043 CATATGGGTAGAGATATATTTTC 4066
 RESULT 4
 AA40887
 ID AA40887 standard; cDNA; 6254 BP.
 AC
 AA40887;
 XX
 AC
 AA40887;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Coding sequence of clone CO722_1.
 XX
 DE Human; nutritional supplement; cell proliferation/differentiation;
 KW cytokine; immunostimulant; immunosuppressant; haematopoiesis regulator;
 KW receptor/ligand activity; cadherin/tumour invasion suppressor;
 KW anti-inflammatory; tumour inhibitor; clone CO722_1; da.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH CDS 383..3961
 FT /*tag= a
 FT /product= "clone CO722_1"
 FT /note= "no stop codon given"
 XX
 XX MO9824905-A2.

PD 11-JUN-1998.
XX 05-DEC-1997; 97MO-US022211.
PF 06-DEC-1996; 96US-00762216.
PR 03-DEC-1997; 97US-00984516.
XX (GEMV) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agoestino MO;
XX MPI; 1998-333324/29.
DR P-PSDB; AAM57900.
XX
PT New isolated polynucleotides encoding secreted polypeptides - isolated
PT from a human foetal kidney cDNA library, a human adult blood cDNA library
PT or a human adult brain cDNA library.
XX
PS Claim 35; Page 77-81; 109pp; English.
XX
CC This sequence represents the coding sequence of clone CO722_1 of the
CC invention. This clone was isolated from a human adult brain cDNA library.
CC The DNAs and proteins can be used as nutritional sources or supplements,
CC or may exhibit cytokine and cell proliferation/differentiation activity,
CC immune stimulating or suppressing activity, haematopoiesis regulating
CC activity, receptor/ligand activity, anti-inflammatory activity,
CC cadherin/tumour invasion suppressor activity, tumour inhibition activity
CC or other activities
XX
SQ Sequence 6254 BP; 1978 A; 1274 C; 1293 G; 1704 T; 0 U; 5 Other;

Query Match 80.2%; Score 3316; DB 2; Length 6254;
Best Local Similarity 90.2%; Freq. No. 0;
Matches 3758; Conservative 0; Mismatches 10; Indels 396; Gaps 4;

QY 1 CTTCAAGTTCCTCCGATGAAATTAATTAAGTTCAGACACAGCTTTCAGAAATCTT 60
DB 269 CTTCAAGTTCCTCCGATGAAATTAATTAAGTTCAGACACAGCTTTCAGAAATCTT 328
QY 61 TTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 329 TTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 388
QY 121 CTTAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 389 CTTAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448
QY 181 CTGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 449 CTGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
QY 241 GTTACAGCTTCCAAACATCAACCAACAGTCTCAAAAGATTATATGACCTTCGGAG 300
DB 509 GTTACAGCTTCCAAACATCAACCAACAGTCTCAAAAGATTATATGACCTTCGGAG 568
QY 301 AATATTGTAATCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 569 AATATTGTAATCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628
QY 361 AATGGGAGCTATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 629 AATGGGAGCTATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
QY 421 AGCTCATATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 480
DB 689 AGCTCATATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 748
QY 481 TGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 749 TGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808
QY 541 AGATCACTATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

DB 809 AGATCACTATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
QY 601 TTAGTACTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 869 TTAGTACTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
QY 661 AATTCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 929 AATTCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 988
QY 721 TATTTTCCATGTCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 989 TATTTTCCATGTCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
QY 781 AATCATCTCAACATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 1049 AATCATCTCAACATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1102
QY 841 GAATGAATGACATATAGCTGTAATTTAGTGAACATGATTTATGCTAAATCA 900
DB 1103 -----GTAATCA 1111
QY 901 AGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 1112 AGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1171
QY 961 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 1172 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
QY 1021 TACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1232 TACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1291
QY 1081 AAAACCTTGACATATTCATGATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1292 AAAACCTTGACATATTCATGATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1351
QY 1141 AAAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1352 AAAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 1201 TGGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1412 TGGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471
QY 1261 AGAGCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1472 AGAGCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1531
QY 1321 ATTGCCCTGATGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1532 ATTGCCCTGATGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1591
QY 1381 CAAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1592 CAAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1651
QY 1441 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1652 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1711
QY 1501 CTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1712 CTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1771
QY 1561 CTCCCAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1772 CTCCCAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1831
QY 1621 GTTTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

Db 1832 GTTTTACATGAAATGAACTTTG-----GAAATT 1861
QY 1681 CCTGTGGCCCAAAAGGACAGTACAGAACTTATACGTGTTCAGAGAAATTAATTAAGG 1740
Db 1862 CCTGTGGCCCAAAAGGACAGTACAGAACTTATACGTGTTCAGAGAAATTAATTAAGG 1921
QY 1741 ATGGCAAGAAATGAACTTCACTT-----ACAGCCC 1770
Db 1922 ATGGCAAGAAATGAACTTCACTTAAATCAAAAGATGCTACATGATCGTTAAACAGCCC 1981
QY 1771 GAAATGCACTGTGTGAAAGAGAGACATGCTCCTTTGAATGCAAACTGAAACATGAT 1830
Db 1982 GAAATGCACTGTGTGAAAGAGAGACATGCTCCTTTGAATGCAAACTGAAACATGAT 2041
QY 1831 CACACCTTATCCCTCACTGTCTGTGGCTGAGAGCAACAGGAACTGCCAGTGAATGA 1890
Db 2042 CACACCTTATCCCTCACTGTCTGTGGCTGAGAGCAACAGGAACTGCCAGTGAATGA 2101
QY 1891 AGGTTCACTGTGTGCAAGAGATCATAGTGTGATGCTGATGTCAGTACGATGACAGCGG 1950
Db 2102 AGGTTCACTGTGTGCAAGAGATCATAGTGTGATGCTGATGTCAGTACGATGACAGCGG 2161
QY 1951 ACCTACAGCTGTGTGGCCCAACACCACTTGTGACAGCTCTCCGCCAGCGCTGTCTTAC 2010
Db 2162 ACCTACAGCTGTGTGGCCCAACACCACTTGTGACAGCTCTCCGCCAGCGCTGTCTTAC 2221
QY 2011 GTTGTGTCTCTACTCACTCACTCAGCTCCGTTTACATGATGCTCCCAATCCTCCTTGA 2070
Db 2222 GTTGTGTCTCTACTCACTCACTCAGCTCCGTTTACATGATGCTCCCAATCCTCCTTGA 2281
QY 2071 TTAGAACTGACAGATCACTTGCACAAAGTGTTCAGCTGTCACTGACCCAGCGCATGAC 2130
Db 2282 TTAGAACTGACAGATCACTTGCACAAAGTGTTCAGCTGTCACTGACCCAGCGCATGAC 2341
QY 2131 AACCAATAGCCCTTTCACAAATTCATCATGAAATGAAATGCAATGCAACAGCCAGG 2190
Db 2342 AACCAATAGCCCTTTCACAAATTCATCATGAAATGAAATGCAATGCAACAGCCAGG 2401
QY 2191 CTGTGGCAACCACTGAACTGAACTTGTGAAACACAGACCAAGCCAGCTGAAGCTGTCT 2250
Db 2402 CTGTGGCAACCACTGAACTGAACTTGTGAAACACAGACCAAGCCAGCTGAAGCTGTCT 2461
QY 2251 CCTTACGTGAACCTACTCTTCCGCGTATGAGAGTGAACAGCATTTGGAAAGCTTGGCC 2310
Db 2462 CCTTACGTGAACCTACTCTTCCGCGTATGAGAGTGAACAGCATTTGGAAAGCTTGGCC 2521
QY 2311 AGCGAGGCGCTGTGAGCATTTTGAAGAAAGCTTCAAGACCAATTAACCCCAACAGCT 2370
Db 2522 AGCGAGGCGCTGTGAGCATTTTGAAGAAAGCTTCAAGACCAATTAACCCCAACAGCT 2581
QY 2371 GTGGAGAGACTGGGATCAGAGCTGTATTTTGAAGATTAACGTGAAGCCCTTGAATGCT 2430
Db 2582 GTGGAGAGACTGGGATCAGAGCTGTATTTTGAAGATTAACGTGAAGCCCTTGAATGCT 2641
QY 2431 TTTCGAATCTAATGAGGCGAGGCTTTCATGACAAAGTTAGCTGGCGCCAGAAAGATGTGAT 2490
Db 2642 TTTCGAATCTAATGAGGCGAGGCTTTCATGACAAAGTTAGCTGGCGCCAGAAAGATGTGAT 2701
QY 2491 GATGAATGACATCTGTGTGTGTGTGCAATGTATTCGAATATTTGTCTCAGGACGCCA 2550
Db 2702 GATGAATGACATCTGTGTGTGTGTGCAATGTATTCGAATATTTGTCTCAGGACGCCA 2761
QY 2551 ACCTTGTTCACATCACTGATGCAAGTTCAAGGCGCTGAATGACATGAGGATTTGCCCCGAG 2610
Db 2762 ACCTTGTTCACATCACTGATGCAAGTTCAAGGCGCTGAATGACATGAGGATTTGCCCCGAG 2821
QY 2611 CCAGCTGTATGTCATGAGGACATTTCTGAGAGAAAGCTTCCCAATGCTGCTCTGGGAACTGT 2670
Db 2822 CCAGCTGTATGTCATGAGGACATTTCTGAGAGAAAGCTTCCCAATGCTGCTCTGGGAACTGT 2881
QY 2671 CGTGTGAATGTGTGAAACAGTACCTTAGCCGAGGTGACCTGGGACCCAGTACTCTTGAA 2730
Db 2882 CGTGTGAATGTGTGAAACAGTACCTTAGCCGAGGTGACCTGGGACCCAGTACTCTTGAA 2941

QY 2731 AGCATCCGAGGACACCTACAAAGGCTATCGAATTTATCTATGGAAGACCCAGAGTTCACT 2790
Db 2942 AGCATCCGAGGACACCTACAAAGGCTATCGAATTTATCTATGGAAGACCCAGAGTTCACT 3001
QY 2791 AAAAGAAACAGACCTGACATTTGAGAAAAGATCCTCACCCTTCCAGGAGAGACCTAT 2850
Db 3002 AAAAGAAACAGACCTGACATTTGAGAAAAGATCCTCACCCTTCCAGGAGAGACCTAT 3061
QY 2851 GGCATGTGGCGGGGCTAGAGGCTTTAGCCACTACACTGAATGTCCGAGTGTCAAT 2910
Db 3062 GGCATGTGGCGGGGCTAGAGGCTTTAGCCACTACACTGAATGTCCGAGTGTCAAT 3121
QY 2911 GGGAAAGGGAGGGGCGCCAGCCAGCTGACAGAGTCTTTAATATCTCAGAAAGAGTCCCC 2970
Db 3122 GGGAAAGGGAGGGGCGCCAGCCAGCTGACAGAGTCTTTAATATCTCAGAAAGAGTCCCC 3181
QY 2971 AGTGTCTCCCTGTCTTTGAAATGTGAAATCCAAACATGACCTCTCTCACTTTGGAATGG 3030
Db 3182 AGTGTCTCCCTGTCTTTGAAATGTGAAATCCAAACATGACCTCTCTCACTTTGGAATGG 3241
QY 3031 GATCCACGAGCCACCCGATGATGATTTGACAGAGTACACCTTAAAGTATCAGCAAT 3090
Db 3242 GATCCACGAGCCACCCGATGATGATTTGACAGAGTACACCTTAAAGTATCAGCAAT 3301
QY 3091 AACAGCAACATGAATTAAGGCTCTGTGTGATTTGAAATTCCTGCCAACAGACAGG 3150
Db 3302 AACAGCAACATGAATTAAGGCTCTGTGTGATTTGAAATTCCTGCCAACAGACAGG 3361
QY 3151 TGGACTTTTAAATTTAAATTTTCACTGACATGATTAAGTTTATTTATGACAAACA 3210
Db 3362 TGGACTTTTAAATTTAAATTTTCACTGACATGATTAAGTTTATTTATGACAAACA 3421
QY 3211 TCAGCAGATGACGAAGTCAATTTACAGAGAAAGAGTAAACAACCTGATGAAGCTGAT 3270
Db 3422 TCAGCAGATGACGAAGTCAATTTACAGAGAAAGAGTAAACAACCTGATGAAGCTGAT 3481
QY 3271 ATTCTTCCACCTGATGATGATGACAGCAAAAGTTCAAGCTGTAATACAGATCAGCAAT 3330
Db 3482 ATTCTTCCACCTGATGATGATGACAGCAAAAGTTCAAGCTGTAATACAGATCAGCAAT 3510
QY 3331 CTTAATGCTGACGCTGACGCTGACATGATGCAATATCACTTGGGAATATGAGGACCAAG 3390
Db 3511 ----- 3510
QY 3391 CATGTGAACCTTATGTTGAATATGATGTGATGACAGGACAGAAAGAAATGAGAAAGA 3450
Db 3511 ----- 3510
QY 3451 ATTGTAAATGATTTCTCGAGCTTCTTTGGGTTAAAGGCTTAATGACAGAAACAGCATAC 3510
Db 3511 ----- 3510
QY 3511 AAAATTCAGATTTGCTGTGTGGGAGCTCTGTGTTTGTGATTTCAAGAGATGTGTTGAG 3570
Db 3511 ----- 3510
QY 3571 ACAGGCGCAGGATGAGCAAGCCGAGAGGTGATTTGCAACTCAGGGCTGTTCTTGGT 3630
Db 3511 -----AGCATGCAAGCCGAGAGGTGATTTGCAACTCAGGGCTGTTCTTGGT 3562
QY 3631 CTGATGTGCTGTGCTCTCTCTTATCTTAATTTTGTGATTTGCTTCACTCAGAGA 3690
Db 3562 -----AGCATGCAAGCCGAGAGGTGATTTGCAACTCAGGGCTGTTCTTGGT 3622
QY 3691 AACAAAGGTGTAAATATTCAGTTAAAGAAAGAAATGCCATGCTGACCTGAAATC 3750
Db 3622 AACAAAGGTGTAAATATTCAGTTAAAGAAAGAAATGCCATGCTGACCTGAAATC 3682
QY 3751 CAGCTTACAGAAAGATGATGAGCACTTTGAGAAATACAGTATGACAGAGACCAAG 3810
Db 3682 CAGCTTACAGAAAGATGATGAGCACTTTGAGAAATACAGTATGACAGAGACCAAG 3742

QY 3811 CCTTTGAAAAAGAGTGCACCTCTTCAGACAGACTGTGAAAAAGATAGTGC 3870
 DB 3743 CTTTGAAGAAAAAGAGTGCACCTCTTCAGACAGACTGTGAAAAAGATAGTGC 3802
 QY 3871 GACAGCCCTAGTGTACTATGAGAGAGGGGTTAATGCGCAGTTCAATGAGATGCTCTTT 3930
 DB 3803 GACAGCCCTAGTGTACTATGAGAGAGGGGTTAATGCGCAGTTCAATGAGATGCTCTTT 3862
 QY 3931 ATTGGAACAATACAGTGTGTAAGAAAGAAAGACCCGCTGAAGAAACGAACCTCAG 3990
 DB 3863 ATTGGAACAATACAGTGTGTAAGAAAGAAAGACCCGCTGAAGAAACGAACCTCAG 3922
 QY 3991 GCACTCTCTCTCTCAACGCCATGAATTCCTTTGTTAATTTTAAGTCAAAAGCAATA 4050
 DB 3923 GCACTCTCTCTCTCAACGCCATGAATTCCTTTGTTAATTTTAAGTCTTTGCCAATA 3982
 QY 4051 TTCATTTCTCTGAAATGTTATCTTAAGCTCTTTGTTGTCAGCCCTCTCAATCTATGAA 4110
 DB 3983 TTCATTTCTCTGAAATGTTATCTTAAGCACTGTTTTCAGCCCTCTCAATCTATGAA 4042
 QY 4111 CATATGGGTAGAGATATATTTTC 4134
 DB 4043 CATATGGGTAGAGATATATTTTC 4066

RESULT 5

AAF98452 standard; cDNA; 6254 BP.

AAF98452;

07-JUN-2001 (first entry)

Human cDNA clone CO722_1 sequence SEQ ID 129.

Human; secreted protein; nutrient; cytokine modulator; proliferation;
 differentiation; immune system modulator; tissue growth; chemotactic;
 haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 haematopoiesis.

Homo sapiens.

MO20011988-A1.

22-MAR-2001.

14-SEP-2000; 2000MO-US025135.

17-SEP-1999; 99US-00398829.

(GENY) GENETICS INST INC.

Jacob K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

Merberg D, Treacy M, Bowman KR, Spaulding V, Agostino MJ;

MPI: 2001-244801/25.

P-PSDB; AAB90717.

Isolated nucleic acids encoding polypeptides, useful for modulating e.g.

cytokine and cell proliferation/differentiation activity, the immune

system and hemopoiesis regulating activity.

Claim 12, Page 456-458; 557BP; English.

Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 tissue types, and may be used in the prevention, treatment and diagnosis
 of diseases associated with inappropriate protein expression. The
 polypeptides and nucleic acids may be used as nutrients or to modulate
 cytokine and cell proliferation/differentiation activity and may also be
 involved in modulation of the immune system. The cDNA sequences,
 proteins, their agonists and/or antagonists exhibit haematopoiesis
 regulating activity; tissue growth activity; activin/inhibin activity;

CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
 CC activity. Included in the invention are probes represented in AAF98490 -
 CC AAF98572 which are specific for the cDNA clones encoding the secreted
 CC proteins
 XX

SO Sequence 6254 BP; 1978 A; 1274 C; 1293 G; 1704 T; 0 U; 5 Other;

Query Match 80.2%; Score 3316; DB 5; Length 6254;

Best Local Similarity 90.2%; Pred. No. 0; Mismatches 10; Indels 396; Gaps 4;

Matches 3758; Conservative 0;

QY 1 CTTCAAAGTCCCGCATGATAAATTAAGTTGACACAGATTTCAGAAAATCTT 60
 DB 269 CTTCAAAGTCCCGCATGATAAATTAAGTTGACACAGATTTCAGAAAATCTT 328
 QY 61 TTGTGAAGAGAAAAAGAAATTCAGTGTGTAGTCTCAGCAGAGATTAAAGTAAAGC 120
 DB 329 TTGTGAAGAGAAAAAGAAATTCAGTGTGTAGTCTCAGCAGAGATTAAAGTAAAGC 388
 QY 121 CTTAAATATATGCGGAAAAAGAGGCTTATCTGGGGCAGAGTCCCTGATTTCTTTC 180
 DB 389 CTTAAATATATGCGGAAAAAGAGGCTTATCTGGGGCAGAGTCCCTGATTTCTTTC 448
 QY 181 CTGTGCAAGATGATTAGTGCATGGAAGTACCTCTTGAATCCAAAATCTTGAAGACTTG 240
 DB 449 CTGTGCAAGATGATTAGTGCATGGAAGTACCTCTTGAATCCAAAATCTTGAAGACTTG 508
 QY 241 GTACAGCCTCCACCATCAACCCAGACGTCTCCAAAAGATTACATTATGACCTCGGGAG 300
 DB 509 GTACAGCCTCCACCATCAACCCAGACGTCTCCAAAAGATTACATTATGACCTCGGGAG 568
 QY 301 AATATTGTATATCAAGTGTGAAAGCCAAAGGAAACCGCCCAAGCTTTTCTGACCCGT 360
 DB 569 AATATTGTATATCAAGTGTGAAAGCCAAAGGAAACCGCCCAAGCTTTTCTGACCCGT 628
 QY 361 AATGGAGCATTTTGAACATGATTAAGACCTCTGTGTACATGAGCTGGACAGGA 420
 DB 629 AATGGAGCATTTTGAACATGATTAAGACCTCTGTGTACATGAGCTGGACAGGA 688
 QY 421 ACGCTCATATTAATCATCATGAGCGAAGGAAAGTGAAGCTTAAGAGATCTATCAG 480
 DB 689 ACGCTCATATTAATCATCATGAGCGAAGGAAAGTGAAGCTTAAGAGATCTATCAG 748
 QY 481 TGTACAGCAAGAGAGAGCGGAGCTGAGTTTCTAATACATTTGTTCCGCCCATCC 540
 DB 749 TGTACAGCAAGAGAGAGCGGAGCTGAGTTTCTAATACATTTGTTCCGCCCATCC 808
 QY 541 AATACACCATTTGTGACCAAAAGAAACCTGAACCAATCAACTTCAAAAGTGTGAGTCT 600
 DB 809 AATACACCATTTGTGACCAAAAGAAACCTGAACCAATCAACTTCAAAAGTGTGAGTCT 868
 QY 601 TTAGTACTTCCCTGAGAGACCCCAATTTGATTAACCAACCACTATATATTTTGGATGAT 660
 DB 869 TTAGTACTTCCCTGAGAGACCCCAATTTGATTAACCAACCACTATATATTTTGGATGAT 928
 QY 661 AATTCCTTTCAAAAGCTTCCAAAGTGAAGAGATTCTCAAGGTTTGAATGGGACCTT 720
 DB 929 AATTCCTTTCAAAAGCTTCCAAAGTGAAGAGATTCTCAAGGTTTGAATGGGACCTT 988
 QY 721 TATTTTTCGAATGTCTCCCAAGAGACACCCGCAAGACTATATCTGTATCTGATTT 780
 DB 989 TATTTTTCGAATGTCTCCCAAGAGACACCCGCAAGACTATATCTGTATCTGATTT 1048
 QY 781 AATCACTACCAACATACAGAGAGCACTATTTCTGTGAAGTATTTCACTGAT 840
 DB 1049 AATCACTACCAACATACAGAGAGCACTATTTCTGTGAAGTATTTCACTGAT 1102
 QY 841 GAATGAATGACATATATGCTCTAATTTGAGTGAAGTGAAGTTTATGCTTAAATCA 900
 DB 1103 -----GCTAAATCA 1111

901 AGTAGAGAGGCGACCAACATTTTAACTCCAGAAAGCAATGCAAGTAACAAGAGAA 960
1112 AGTAGAGAGGCGACCAACATTTTAACTCCAGAAAGCAATGCAAGTAACAAGAGAA 1171
961 TTAAGAGAAATGTGCTTTCACTGAGTGCAATGCAAGAGACTGCTTACCCCAATTAT 1020
1172 TTAAGAGAAATGTGCTTTCACTGAGTGCAATGCAAGAGACTGCTTACCCCAATTAT 1231
1021 TACTGGGCAAAAGGAATGGAATGTACCAAAAACAGGACGTTTATAGAACTTTGAG 1080
1232 TACTGGGCAAAAGGAATGGAATGTACCAAAAACAGGACGTTTATAGAACTTTGAG 1291
1081 AAAACCTGCAAGTCAATTCATGTTTCAAGAGCACTGTGAAATTAACAAATGATAGCA 1140
1292 AAAACCTGCAAGTCAATTCATGTTTCAAGAGCACTGTGAAATTAACAAATGATAGCA 1351
1141 AAAAATGCAATTAGAGCCATCCACCATTCATTTCTGTTAGATTAAAGCGGTCCATAC 1200
1352 AAAAATGCAATTAGAGCCATCCACCATTCATTTCTGTTAGATTAAAGCGGTCCATAC 1411
1201 TGGATCAGAGCCCTGCAAAATCTTGCTGTGCTCCAGAGAGAGATGGAGCCTTGATCTGC 1260
1412 TGGATCAGAGCCCTGCAAAATCTTGCTGTGCTCCAGAGAGAGATGGAGCCTTGATCTGC 1471
1261 AGAGCTAATGCGCAACCCCAAAACCCAGAAATTAGCTGTGTTAACAAATGAGATCCCAATGAA 1320
1472 AGAGCTAATGCGCAACCCCAAAACCCAGAAATTAGCTGTGTTAACAAATGAGATCCCAATGAA 1531
1321 ATTGCCCCCTGATGACCCCGACAGAAATATGATGGGATACCATTTATTTTCAATGTT 1380
1532 ATTGCCCCCTGATGACCCCGACAGAAATATGATGGGATACCATTTATTTTCAATGTT 1591
1381 CAAGAAGATCAAGTCAATGATATCATGTGCAATGCTTAATGAATGGAATTTACTAG 1440
1592 CAAGAAGATCAAGTCAATGATATCATGTGCAATGCTTAATGAATGGAATTTACTAG 1651
1441 GCAAAGCATTTTGTAAATGTGCTGAGCCAGCAACGAATCTTCAACCTGCAACACAC 1500
1652 GCAAAGCATTTTGTAAATGTGCTGAGCCAGCAACGAATCTTCAACCTGCAACACAC 1711
1501 CTCTACCAAGTCAATGCAACAGGCTGCTTTCATGACCTGTGCTTCTTTGGGTCTCCT 1560
1712 CTCTACCAAGTCAATGCAACAGGCTGCTTTCATGACCTGTGCTTCTTTGGGTCTCCT 1771
1561 CTCCCAACCATGAGTGTGTTAAAGAGCTAAAGGAAGTCTCTCATGAAATATTTAT 1620
1772 CTCCCAACCATGAGTGTGTTAAAGAGCTAAAGGAAGTCTCTCATGAAATATTTAT 1831
1621 GTTTTACATGAAATGGAATCTTTGAAATCAAAAGATGCTACATGATCGTTAAAGAAAT 1680
1832 GTTTTACATGAAATGGAATCTTTG-----GAAATTT 1861
1681 CCTGTGGCCCAAAAGACAGTACAGGAATTAATACGTGTGTTGCAAGAAATTAATAGGG 1740
1862 CCTGTGGCCCAAAAGACAGTACAGGAATTAATACGTGTGTTGCAAGAAATTAATAGGG 1921
1741 ATGGCAAAAGAAATGAAGTTCACTT-----ACAGCCC 1770
1922 ATGGCAAAAGAAATGAAGTTCACTTAAAGATGCTACATGATCGTTAAACAGCCC 1981
1771 GAATATGCAAGTGTGCAAAAGAGGAGAGCATGTGCTCTTTGAATGCAAGTGAACATGAT 1830
1982 GAATATGCAAGTGTGCAAAAGAGGAGAGCATGTGCTCTTTGAATGCAAGTGAACATGAT 2041
1831 CACACCTTATCCTCACTGTCTGTGCTGAGAGCAACAGGAACTGCCAGTGTATGAA 1890
2042 CACACCTTATCCTCACTGTCTGTGCTGAGAGCAACAGGAACTGCCAGTGTATGAA 2101
1891 AGGTTCATCTGTTGCAAGAGATCAATTAAGTGTAGCTGATGTCATGATGACAGAGGG 1950
2102 AGGTTCATCTGTTGCAAGAGATCAATTAAGTGTAGCTGATGTCATGATGACAGAGGG 2161
1951 ACCTACAGTGTGTGCGCAACACACTGTGACAGCGTCTCGCCAGCGCTGTGCTTAGC 2010

2162 ACCTACAGTGTGTGCGCAACACACTGTGACAGCGTCTCGCCAGCGCTGTGCTTAGC 2221
2011 GTTGTGTGCTTCTTCACTCCAACTCCAGCTCCGTTTACATGATGCCAAATCTCCCTTAGC 2070
2222 GTTGTGTGCTTCTTCACTCCAACTCCAGCTCCGTTTACATGATGCCAAATCTCCCTTAGC 2281
2071 TTAGAATGACAGATCAACTGCAAAAGTGTTCAGTGTGATGAGACCCAGCGATGAC 2130
2282 TTAGAATGACAGATCAACTGCAAAAGTGTTCAGTGTGATGAGACCCAGCGATGAC 2341
2131 AACATAGCCCATTTACAAATTTCAATTCATTCGAATTTGAATGCAATGCAACAGCAAGG 2190
2342 AACATAGCCCATTTACAAATTTCAATTCGAATTTGAATGCAATGCAACAGCAAGG 2401
2191 CTGTGACACCAACCAATGAAATTTCTGAAACACAGACAGCCAGCTGAGCTGTCT 2250
2402 CTGTGACACCAACCAATGAAATTTCTGAAACAGACAGCCAGCTGAGCTGTCT 2461
2251 CCTTACGTGAATCTCTTCCGCGTGAATGAGTGAACAGCATTTGGAGAGCTTGGCC 2310
2462 CCTTACGTGAATCTCTTCCGCGTGAATGAGTGAACAGCATTTGGAGAGCTTGGCC 2521
2311 AGCGAGGCTCTGACAGATTTTGAAGAAAGCTTCAAGAACAGATTAACCCCAAGCT 2370
2522 AGCGAGGCTCTGACAGATTTTGAAGAAAGCTTCAAGAACAGATTAACCCCAAGCT 2581
2371 GTGGAAGGCTGGGATCAGAGCTGATATTTGAGATTTAGCTGGAAGCCCTTGAATGAT 2430
2582 GTGGAAGGCTGGGATCAGAGCTGATATTTGAGATTTAGCTGGAAGCCCTTGAATGAT 2641
2431 TTGGAATCTAATGAGCGCAGGCTTCAAGTCAAAAGTGAAGTGGCGCCAGAAAGATGAT 2490
2642 TTGGAATCTAATGAGCGCAGGCTTCAAGTCAAAAGTGAAGTGGCGCCAGAAAGATGAT 2701
2491 GATGAATGACATCTGTGTTGTGCAATATGATTCAAATATATTTGTCTCAGGACGCCA 2550
2702 GATGAATGACATCTGTGTTGTGCAATATGATTCAAATATATTTGTCTCAGGACGCCA 2761
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2762 ACCCTTGTTCATACCTGATCAAAAGTTCAGGCTTGAATGACATGAGGGGTTTCCCCCGAG 2821
2611 CCAGCTGATGATGAGGACATTTCTGAGAGAGCTTCCAAATGAGGCTTCTGAGAACGTC 2670
2822 CCAGCTGATGATGAGGACATTTCTGAGAGAGCTTCCAAATGAGGCTTCTGAGAACGTC 2881
2671 CGTGTGAATGTGTGAACAGTACCTTACGCCAGTGTGCACTGGGACCCAGTACTCTGAAA 2730
2882 CGTGTGAATGTGTGAACAGTACCTTACGCCAGTGTGCACTGGGACCCAGTACTCTGAAA 2941
2731 AGCATCCAGAGCACCTACAAAGCTATCGATTTTATGGAAGACCCAGAGTTCATCT 2790
2942 AGCATCCAGAGCACCTACAAAGCTATCGATTTTATGGAAGACCCAGAGTTCATCT 3001
2791 AAAAGAAACAGACGTACATTTGAAAGAAAGATCTTCACTTCCAAAGCAGCAAGCTCAT 2850
3002 AAAAGAAACAGACGTACATTTGAAAGAAAGATCTTCACTTCCAAAGCAGCAAGCTCAT 3061
2851 GGCATGTTCGCGGGGTGAGAGCCCTTTAGCCCTACACATGAAATGTCGAGATGTCAT 2910
3062 GGCATGTTCGCGGGGTGAGAGCCCTTTAGCCCTACACATGAAATGTCGAGATGTCAT 3121
2911 GGGAAAGGGGAGGGCCAGCGAGCCCTGACAGATCTTAAATCTCAAGAAAGATGTCGCC 2970
3122 GGGAAAGGGGAGGGCCAGCGAGCCCTGACAGATCTTAAATCTCAAGAAAGATGTCGCC 3181
2971 AGTGTCTCCTGCTCTTGAAGATTTGATATCCAACTGAGCTCTCTCACTTTGAATGG 3030
3182 AGTGTCTCCTGCTCTTGAAGATTTGATATCCAACTGAGCTCTCTCACTTTGAATGG 3241
3031 GATCCACGAGCCACCCGATGAGCATTTTGAAGATGATCACTTAAAGTATCAGCCAAAT 3090

||||| 5808 CTTAAATAATGCGAAAAAGGCTTATGCGGGGAGAGTGCCCGCTGATTCCTTC 5749
||||| 181 CTGTGCAATGATTTGTGCACTGGAAGTACCTCTTGATCCAAACTCTTGAAGCTTG 240
||||| 5748 CTGTGCAATGATTTGTGCACTGGAAGTACCTCTTGATCCAAACTCTTGAAGCTTG 5689
241 GTACAGCTCCAAACGATCAACCAAGCTCTCCAAAGATTACATTATGACCTCGGGAG 300
5688 GTACAGCTCCAAACGATCAACCAAGCTCTCCAAAGATTACATTATGACCTCGGGAG 5629
301 AATATTGTAATCCAGTGTGAGGCAAGGAAACCGCCCAAGCTTTTCTGGAACCGT 360
5628 AATATTGTAATCCAGTGTGAGGCAAGGAAACCGCCCAAGCTTTTCTGGAACCGT 5569
361 AATGGAGCTCATTTTGAACATCGATAAAGACCTCTGTGTCACTGAAAGCTTGCAAGAA 420
5568 AATGGAGCTCATTTTGAACATCGATAAAGACCTCTGTGTCACTGAAAGCTTGCAAGAA 5509
421 AGGCTCATATTAAATCATGATGAGGAAAGGAAAGCTGAGACCTATGAGAGTCTATCAG 480
5508 AGGCTCATATTAAATCATGATGAGGAAAGGAAAGCTGAGACCTATGAGAGTCTATCAG 5449
481 TGTACAGCAAGGAACGAACGCGAGCTGCAATTCTAATAACATTTGTCCGCCATCC 540
5448 TGTACAGCAAGGAACGAACGCGAGCTGCAATTCTAATAACATTTGTCCGCCATCC 5389
541 AGATCCATCTGTGAGCCAAAGAAAACCTTGAAACCAATCACTTCGAAAGTGTCTGCT 600
5388 AGATCCATCTGTGAGCCAAAGAAAACCTTGAAACCAATCACTTCGAAAGTGTCTGCT 5329
601 TTAGTACTTCCCGCAGACCCCAATTTGATTCACACCTATTAATTTTGGATGAT 660
5328 TTAGTACTTCCCGCAGACCCCAATTTGATTCACACCTATTAATTTTGGATGAT 5269
661 AATTCCTTTCAAGACTTCCAAAGATGAGAGATTTCTCAAGGTTGAATGGAGACCTT 720
5268 AATTCCTTTCAAGACTTCCAAAGATGAGAGATTTCTCAAGGTTGAATGGAGACCTT 5209
721 TATTTTCCAAATCTCTCCAGAGCAACCCGGAAGACTATTCGTGTTATGCTAATTT 780
5208 TATTTTCCAAATCTCTCCAGAGCAACCCGGAAGACTATTCGTGTTATGCTAATTT 5149
781 AATCATACTCAACCAATACAGAGAGCAACCTATTCTGTGAGAGGATTCAGTGAT 840
5148 AATCATACTCAACCAATACAGAGAGCAACCTATTCTGTGAGAGGATTCAGTGAT 5095
841 GAATTGAATGACATAGCTGCTAATTGAGTGAACAGCTGATTTATGGTGTAAATCA 900
5094 -----GCTAATCA 5086
901 AGTAGAGAGGCGCAACCAATTTTAACTCCAGAAAGCAATGCAAGTAAACAAAGGAA 960
5085 AGTAGAGAGGCGCAACCAATTTTAACTCCAGAAAGCAATGCAAGTAAACAAAGGAA 5026
961 TTAAGAGGAAATGTGCTTCACTGAGAGTGAAGGAGTGTGCTACCCCAATTTAT 1020
5025 TTAAGAGGAAATGTGCTTCACTGAGAGTGAAGGAGTGTGCTACCCCAATTTAT 4966
1021 TACTGGGCAAAAGAGATGGAATGCTAACCCAAAAGAGACAGTTTATAAGAACTTTGAG 1080
4965 TACTGGGCAAAAGAGATGGAATGCTAACCCAAAAGAGACAGTTTATAAGAACTTTGAG 4906
1081 AAAACCTTGAGATCATCTATGTTTGAAGAGAGACTCTGGAATTAACAAATGTAAGCA 1140
4905 AAAACCTTGAGATCATCTATGTTTGAAGAGAGACTCTGGAATTAACAAATGTAAGCA 4846
1141 AAAATGCAATTTAGAGCATCAACATACATTTCTGTTAGATTAAAGGAGCTCCATAC 1200
4845 AAAATGCAATTTAGAGCATCAACATACATTTCTGTTAGATTAAAGGAGCTCCATAC 4786
1201 TGGATCAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGACCTTGATCTGC 1260

Db 4785 TGGATCAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGAGCTTGATCTGC 4726
Qy 1261 AGAGCTAATGGCAACCCCAACCCAGAAATTAAGTGTGTTAAACAAATGAGTCCCAATAGAA 1320
Db 4725 AGAGCTAATGGCAACCCCAACCCAGAAATTAAGTGTGTTAAACAAATGAGTCCCAATAGAA 4666
Qy 1321 ATTTGCCCTGATGACCCCAAGAGAAATTAAGTGTGTTAAACAAATGAGTCCCAATAGAA 1380
Db 4665 ATTTGCCCTGATGACCCCAAGAGAAATTAAGTGTGTTAAACAAATGAGTCCCAATAGAA 4606
Qy 1381 CAAGAAAGATCAAGTGCATATATGAGTGAATGCTCTTAATGAATATGATATTACTG 1440
Db 4605 CAAGAAAGATCAAGTGCATATATGAGTGAATGCTCTTAATGAATATGATATTACTG 4546
1441 GCAAAAGCATTTGTAATGTGTGCTGAGGCAACCAAGAAATCTGCAACCTGCAAAACAA 1500
4545 GCAAAAGCATTTGTAATGTGTGCTGAGGCAACCAAGAAATCTGCAACCTGCAAAACAA 4486
Qy 1501 CTCTACAGGTCATTTGCAACAGGCTGCTTTTACTGACCTGTCTCTTCTTGTGGTCTCT 1560
Db 4485 CTCTACAGGTCATTTGCAACAGGCTGCTTTTACTGACCTGTCTCTTCTTGTGGTCTCT 4426
Qy 1561 CTCTACAGGTCATTTGCAACAGGCTGCTTTTACTGACCTGTCTCTTCTTGTGGTCTCT 1620
Db 4425 CTCTACAGGTCATTTGCAACAGGCTGCTTTTACTGACCTGTCTCTTCTTGTGGTCTCT 4366
Qy 1621 GTTTTACATGAAATGGAATCTTGGAAATCAAAAGATGCTACATGATCGTTAAAGAAAT 1680
Db 4365 GTTTTACATGAAATGGAATCTTGGAAATCAAAAGATGCTACATGATCGTTAAAGAAAT 4336
Qy 1681 CCTGTGCCCCAAAGAGAGAGTACAGAACTTATACGTGTGTGCAAGAAATTAATTAAGG 1740
Db 4335 CCTGTGCCCCAAAGAGAGAGTACAGAACTTATACGTGTGTGCAAGAAATTAATTAAGG 4276
Qy 1741 ATGGCAAGATGGAATGCTCTT-----AAGGCC 1770
Db 4275 ATGGCAAGATGGAATGCTCTT-----AAGGCC 4216
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Db 4215 GAATATGAGTGTGCAAGAGAGAGAGTGTGCTTTGAATGCAAGTGAATCATGAT 4156
Qy 1831 CAACCTTATCCCTCACTGTCTGTGCTGAAGCAACAGGAACTGCCAGTATGAA 1890
Db 4155 CAACCTTATCCCTCACTGTCTGTGCTGAAGCAACAGGAACTGCCAGTATGAA 4096
Qy 1891 AGGTTCACTGTGCAAGAGATCATGTGTGAGTGTGATGTCAAGTGAACAGCGGG 1950
Db 4095 AGGTTCACTGTGCAAGAGATCATGTGTGAGTGTGATGTCAAGTGAACAGCGGG 4036
Qy 1951 ACCTACAGTGTGTGAGGCAACCACTGAGACAGCTCTCCGAGCGCTGTGCTTAC 2010
Db 4035 ACCTACAGTGTGTGAGGCAACCACTGAGACAGCTCTCCGAGCGCTGTGCTTAC 3976
Qy 2011 GTTGTGTCTCTTACCTCAACCTCAGCTCCGTTTACATGTGCCAAATCTCTCCCTTGA 2070
Db 3975 GTTGTGTCTCTTACCTCAACCTCAGCTCCGTTTACATGTGCCAAATCTCTCCCTTGA 3916
Qy 2071 TTAAGATGAGATCAACCTTGAACAAAGTGTTCAGCTGTCACTGAGACCCAGGCGATGAC 2130
Db 3915 TTAAGATGAGATCAACCTTGAACAAAGTGTTCAGCTGTCACTGAGACCCAGGCGATGAC 3856
Qy 2131 AACCAATAGCCCATTTACAAATTTATCATCGAATATGAAGTGCATGACAGGCAAGG 2190
Db 3855 AACCAATAGCCCATTTACAAATTTATCATCGAATATGAAGTGCATGACAGGCAAGG 3796
Qy 2191 CTGTGGCAACCAACCTGAAGTTTCTGGAACAGAGCAACAGCCAGCTGAAGCTGTCT 2250
Db 3795 CTGTGGCAACCAACCTGAAGTTTCTGGAACAGAGCAACAGCCAGCTGAAGCTGTCT 3736
Qy 2251 CCTTACGTGAATTAATCTCTTCCGCTGATGAGCAAGTGAACAGATTTGGAGAGCTTGGCC 2310
Db 3735 CCTTACGTGAATTAATCTCTTCCGCTGATGAGCAAGTGAACAGATTTGGAGAGCTTGGCC 3676

2311 AGGAGGCGCTGTGAGAGATTTTGAAGAAAGCTTCAGAAACAGATATAAAACCCACAGCT 2370
2371 GTGGAAGAGCTGGAGATCAGAGCTGATTAATTGGAGATTAAGTGAAGCCCTTTGAATGCT 2430
2431 TTGGAATCTAATGAGGCGAGGCTTCAGTACAAAGTTAGCTGGGCGCAGAAAGTGGTAT 2490
2491 GATGAATGAGCAATCTGAGTGTGAGCAATGTATCCAAATATATGTCTCAGGACAGCA 2550
2551 ACCTTTGTTCCATACCTGATTCAAAGTTCAGGCCCTGAATGACATGAGGTTTGGCCCGAG 2610
2611 CCAAGCTGATGATCTGAGGACATTTCTGAGAAAGACCTCCCAATGGTGGCTCTGGGAACGTG 2670
2671 CGTGTGAATGTGGTGAACAGTACCTTAGCCGAGGTGACCTGGGACCCAGTACCTTGAAA 2730
2731 AGCATCCGAGACACCTACAGGCTATCCGATTTTCTATTTGAGAGACCCAGAGTTCATCT 2790
2791 AAAAGAAACAGAGCTCACTTGAAGAAAAGATCTCTCACTTCCAAAGCAGCAAGATCTCAT 2850
2851 GGCATGTCGCGGGGCTAGAGCCCTTTAGCACTACACCTGAATGCCGAGTGCAT 2910
2911 GGGAAAGGGGAGGAGCCAGCAGCAGCCCTGACAGAGTCTTTAATATCTCAGAAAGAGTCCCC 2970
2971 AGTGTCTCCCTCGTCTTTGAAGATTTGAATCCAACTGGACTCTCTCACTTTGGAATGG 3030
3031 GATCCACCGAGCCAGCCGAGATTTGAGACAGATACACCTTAAGATACAGCAAT 3090
3091 AACAGACACATGAATTAAGCCCTCTGTAGATTTGAAAAATTCCTCCAAACAGACAGCG 3150
3151 TGGACTTTAAAAATTTAAATTTTCAACACTCGATATTAAGTTTATTTCTATGCAAAACA 3210
3211 TCAGGAGATCAGGAGTCAAAATTAAGAGAGAGCACTGTAACAATGAGTGAAGTGGT 3270
3271 ATCTTCCACCTGATGTAGGTGAGGCAAAAGTTCAGCTGTAAATCCAGATCAGCAAT 3330
3331 CTTACTGTGACGTGCTGAGACCTATGCCAATATGATTGGAAATAGAGGACCAAG 3390
2722 ----- 2723

3391 CATGTGAACCTTTAATGTTGAATATGTTGTAGAGGACGACGAAAGAAATGAGAAAGAA 3450
2722 ----- 2723
3451 ATTGTAATGTTCTCGAGACTTCTTTGGGTTAAAGGCTTAATGCCAGAAACAGCATAC 3510
2722 ----- 2723
3511 AAAGTTGAGTTGATGTGTGGGAGACTGTGGTTTGTGATTCAGAGGATGTGTTGAG 3570
2722 ----- 2723
3571 ACAGGCCAGCGATGAGGAGCCGAGGATGATATTTGCACTCAGAGCTGTTCATGCT 3630
2722 ----- AGGATGTGAGGAGCCGAGGATGATATTTGCACTCAGAGCTGTTCATGCT 3690
3631 CTGATGTGTGCTGTGCTCTCTCTTATCTTAATTTTGTGATTTGTTGCTTCACTGAGA 3690
2670 CTGATGTGTGCTGTGCTCTCTCTTATCTTAATTTTGTGATTTGTTGCTTCACTGAGA 2611
3691 AACAAAGGTTGATTAATTCAGTTAAAGAAAGAGTGGCCATGCTGACCTGAAATC 3750
2610 AACAAAGGTTGATTAATTCAGTTAAAGAAAGAGTGGCCATGCTGACCTGAAATC 2551
3751 CAGCCTATGAGAGAGATGATGAGCAATTTGAGAGATACAGTATGCAAGAACCAAG 3810
2550 CAGCCTATGAGAGAGATGATGAGCAATTTGAGAGATACAGTATGCAAGAACCAAG 2491
3811 CTTTGAAGAAAGAGTGAATCTCTTCAAGACAGACTGTGAAAAGAAAGATAGTAC 3870
2490 CTTTGAAGAAAGAGTGAATCTCTTCAAGACAGACTGTGAAAAGAAAGATAGTAC 2431
3871 GACAGCTAGTTGATGATGAGAGAGGTTAATGAGCAAGTCAATGAGAGTCTCTT 3930
2430 GACAGCTAGTTGATGATGAGAGAGGTTAATGAGCAAGTCAATGAGAGTCTCTT 2371
3931 ATTGACAAATACAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3990
2370 ATTGACAAATACAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2311
3991 GCACTTCTCTGTGACAGCCATGATTCCTTTGTTAATTTTAAAGTCTTGGCAATA 4050
2310 GCACTTCTCTGTGACAGCCATGATTCCTTTGTTAATTTTAAAGTCTTGGCAATA 2251
4051 TTGCAATTTCTAGAGATGTTATCTTAAGCTCTTGTGAGCCCTCATATATGA 4110
2250 TTGCAATTTCTAGAGATGTTATCTTAAGCACTTGTGTGAGCCCTCATATATGA 2191
4111 CATATGGGTAGAGATATTTTC 4134
2190 CATATGGGTAGAGATATTTTC 2167

RESULT 7
AAS16294
ID AAS16294 strand: cdna, 3943 BP.
XX AAS16294;
AC
XX
DT 14-FEB-2002 (first entry)
XX
XX
DE cdna encoding chicken Nr-CAM.
XX Neurite outgrowth; fibronectin Type III repeat; cell adhesion molecule;
XX F80; Fn3-5; Fn4-5; neurone; peripheral nerve damage; trauma; infarction;
XX degenerative disease; malignant disease; antibacterial;
XX central nervous system lesion; virucide; antiparkinsonian; nootropic;
XX gliosis; neuroprotective; antiinflammatory; chicken; Nr-CAM; ss.
XX
OS Gallus sp.
XX
XX
Key Location/Qualifiers
CDS 33..3839
FT

FT	/*tag= a	
XX	/product= "Nr-CAM"	
FN		
XX		
PD	US613265-B1.	
XX		
XX	06-NOV-2001.	
PF	24-JUL-1995; 95US-00506296.	
XX		
PR	24-JUL-1995; 95US-00506296.	
XX		
PA	(SCRI) SCRIPPS RES INST.	
XX		
PI	Phillips G, Cunningham BA, Crossin KL;	
DR	WPI; 2002-017011/02.	
XX	P-PSDB; AAU10650.	
PT	Polypeptide for promoting neurite out-growth useful for treating diseases	
PT	such as inflammation, Parkinson's disease, trauma, comprises fibronectin	
PT	type III repeats derived from a family of cell adhesion molecules.	
XX		
PS	Example 1; Fig 30; 132pp; English.	
XX		
CC	The present invention relates to polypeptides that promote neurite	
CC	growth. The polypeptides contain fibronectin type III repeats derived	
CC	from a family of cell adhesion molecules (CAMs). The polypeptides of the	
CC	invention include the F80, Fn3-5, and Fn4-5 regions of the CAM family.	
CC	members chicken Ng-CAM, chicken Nr-CAM, mouse LiCAM and human LiCAM. The	
CC	polypeptides of the invention are useful for promoting neurite outgrowth	
CC	of neuronal cells in vitro e.g. in a cell culture system, or in vivo for	
CC	treating disorders such as peripheral nerve damage associated with	
CC	physical or surgical trauma, infection, bacterial or viral infections,	
CC	toxin exposure, degenerative disease, malignant disease that affects	
CC	peripheral or central neurones, or in surgical or transplantation methods	
CC	in which new neuronal cells from brain, spinal cord or dorsal root	
CC	ganglia are introduced and require stimulation of neurite outgrowth from	
CC	the implant and innervation into the recipient tissue, where the diseases	
CC	include central nervous systems lesions, gliosis, Parkinson's disease,	
CC	Alzheimer's disease, gliotic response or inflammation. The present	
CC	sequence encodes for chicken Nr-CAM protein	
XX		
SQ	Sequence 3943 BP; 1279 A; 757 C; 866 G; 1041 T; 0 U; 0 Other;	
	Query Match 54.1%; Score 2236; DB 6; Length 3943;	
	Best Local Similarity 73.7%; Pred. No. 0;	
	Matches 2916; Conservative 0; Mismatches 945; Indels 93; Gaps 2	
QY	98 CAGCAGGAGCTTAAGCTAATGACGACTTAAATATATGCGGAAAGAAAGCCCTTATCTGCGG 157	
DB	1 CAAGAGTGATTTACTAGTAGAGCCTTAAATCATGATGATAAGAGAACATATCTGCAA 60	
QY	158 GGAGAGTGGCCCGATTCCTTCCTCGTGCACATGATTGTGCACTGGAAGTAACTCTTG 217	
DB	61 GGAAGCTTCCTGGTTCCTTCCTTCCTGTCGCAATGATGTTCTGCATTGATGATACCTCTTG 120	
QY	218 ATCCAAAACCTTCTGTAAGACTGGTACAGCTTCGAACCATCAACCCAAAGCTCTCCAAAAG 277	
DB	121 ATTCAAAACCTTCTGTAAGAAATGTCTCAACCTTCGAACATTAATCTACGAGCTCTCCAAAAG 180	
QY	278 ATTACATTATGAGCCCTCGGGAGAAATATTGTATATCCAGTGTGAAGCCAAAGGAAACGCG 337	
DB	181 ATTACATTGTGAGCCCTCGAGAGAAATATTGTATATCAATGTGAAGCAAAAGGAAACCAAC 240	
QY	338 CCCCAAGCTTTTCCTGAGACCCGTAATGGGACATCTTTGACATCGATTAAGAACCTCTGCG 397	
DB	241 CTCCTAGCTTCTCCTGAGACCGCGCAAGGAATCTATTTTATATATGATTAAGATGACACAG 300	
QY	398 TCACCATGAAGCTGGCAGAGGAACGCTCATATATTAACATCATGACGGAAGGAAAGCTG 457	
DB	301 TTAACATGAACCAAAATTCAGGAACCTCTGTTTAATTTATGATATGCTGTGGAAGCGAG 360	
QY	458 AGACCTATGAGAGAGTCTATCACTGTATACAGCAAGAAAGCAACGCGGAGCTGCAATTTCTTA 517	

[illegible]

1384 ACTGTCCTTATTTGGTTCACCTAAGCTGAAATCGAATGTTAGGGAGTGAAGATA 1443
1598 GTGCTCTCATGAAGATTTATTTGTTTACATGAATAATGAACTTGGAAATCAAGATG 1657
1444 GATCTTGGAGGAATGAAATATGTTTTCATATGATATGAACTTGGAAATTCAGTGG 1503
1658 CTACATGATCTGTTAAAGAAATTCGTGGCCCCAAAGACAGTACAGAACTTATACGT 1717
1504 CTCAGAAAGTATGTACTGGCACTACATACATGTTTCAAGAAATTAATTAAGGAACAGC 1563
1718 GTGTTGAAAGAAATTAATTTGGATGGCAAGATGAAGTTCACTTACAGCCCGAATATG 1777
1564 AAATTAAGTACATCTGAAGTTAAAGACCAACGATGATTAATTAACAGCCACAGTACA 1623
1778 CAGTTGCAAGAGGAGAGATGTCCTTTGAATGCAAGGAAGAACTGATCACACCT 1837
1624 AAGTGAATCAAGATCTGCCAGGCTTCATTGAGTGTAAATTAACATGATCTTACCT 1683
1838 TATCCCTCACTGTCGTGGCTGAAAGACAAACAGGAACTGCCAGTATGAAGGTTCA 1897
1684 TAATACCAACAGTATATGCTGAAAGACATATGATACCAAGATGATGAAGGTTTC 1743
1898 CTGTTGACAGAGATCATCTAGTGTAGCTGATGTCACTGACATGACAGCGGACCTTACA 1957
1744 TAGTGTAAAGACAATTGACCATTTATGATGTAATGTAAGATGATGAACATATATA 1803
1958 CGTGTGTGGCAACACACTGTGACAGGCTCTCCGACGCGTGTAGCTTGGTGTG 2017
1804 CTTGACATGTTAAATCTACTCTGACAGGTTTCACAGATGCTGTGCTTACGTGTGG 1863
2018 CTCTCACTCAACTCCAGCTCCCGTTTACGATGTCCCAATCTCTCCCTTGAATTAAGAC 2077
1864 CTGCTCCCACTCCAGCTATATGATTTACCTCGGCAATTCACCGCTTGAATTTGAAAT 1923
2078 TGAAGATCAACTTGAACAAAGTTTCACTGTCTGATGACCCGAGCGATGACACATATA 2137
1924 TGAAGATCAACTTGAACAAAGTTTCACTGTCTGATGACCCGAGCGATGACACATATA 1983
2138 GCGCCATTACAAATTCATCTGATATGAAATGCAATGCAAGCCAGGCTGTGGC 2197
1984 GTCCCACTTACAACTTGTGATGATGAAATGAAATGAACTTACATGAGCCAGGCGTATGAC 2043
2198 ACCGCAAACTGAAGTTTCTGAAACACAGACACAGCCAGCTGAGCTGTCTCTTACG 2257
2044 ATTACAGAGGAAATTCCTGATCTCATACAACTGATACAGTTGAAGTTGTCTCCGATAG 2103
2258 TGAATCTACTCTCCGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2317
2104 TCAACTACTCATCTCCGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2163
2318 CGCTGAGAGATTTTGAAGAAAGCTCAGAACCAATTAACCCCAAGCTGTGGAG 2377
2164 CATGTAACAGTACCTGACAAAGTCCGCAACCCCATGAAATCTTTTAAATGTAAG 2223
2378 GACTGGATCAAGACCTGATTAATTTGGAATTTAGTGAAGCCCTTGAATGTTTGAAT 2437
2224 GATAGGCTCGAACTGATTAATTTGTAATTAACGAGGAGTCTTTAAAGGCTTTCACT 2283
2438 CTAAATGGGCAAGGCTTCACTGATCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2497
2284 CTAAATGGGCAAGGCTTCACTGATTAATTTGTAATTAACGAGGAGTCTTTTGAATGAT 2343
2498 GGAATCTGTGTGTGGCAAAATGATCCAAATTAATTTGTCTCAAGGACGCCAACTTTG 2557
2344 GGAATCTGTGTGTGGCAAAATGATCCAAATTAATTTGTGTGTGTGTGTGTGTGTGTGTGT 2403
2558 TTCCATACCTGATCAAGTTCAGGCTGATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2617
2404 TTCCATACCTGATCAAGTTCAGGCTGATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2463
2618 TAGTCAATGGAATTTGGAAGAAAGCTCCCAATGATGCTCTGTGAAAGCTGTGATGA 2677
2464 AGGTATTTGGAATTTGGAAGAAAGCTCCCAATGATGCTCTGTGAAAGCTGTGATGA 2523

2678 ATGTGTTGAACAGTACCTTACCGAGGTGACCTGGGACCCAGTACTCTGAAGAGATCC 2737
2524 ATGTCTATTACAGCATTGGCAAGGTGCACTGGGACCCCTGTTCACATTAATCTGTCC 2583
2738 GAGAACCTTACAGGCTATCGAATTTACTATTTGAAGACCCAGATTCATCTTAAAGAA 2797
2584 GAGAACCTTACAGGCTATCGAATTTACTATTTGAAGACCCAGATTCATCTTAAAGAA 2643
2798 AAGAGCTCACTTGAAGAAAGATCTCAGCTTCCAGGCGAAGATCTCAGGATGCT 2857
2644 GTAAACGGATGTGAAGAAAGATCTTGAATTTGAAGGAAAGATCTTGAAGT 2703
2858 TCCCGGGCTAGAGCTTTTACCACTACAGTAAATGTCGAGTGTCAATGGGAAAG 2917
2704 TACAGGCTAGAGCTTATGATTTCTTACAGCTAAATGTTAGTGTATATGTTAAAG 2763
2918 GGAAGGCGCCAGCCAGCCCTGACAGAGTCTTTAATCTCCAGAGAGTCCCAAGTCTG 2977
2764 GAGAAAGACCAAGCAAGCCAGCAAGATTTTAAATCTCTGAAGAGTCTTACGCCAC 2823
2978 CCTCGCTTTGAAGATTTGAATCCACACTGAGCTCTCTCACTTTGGAATGGATCCAC 3037
2824 CCTCTTTTGAAGATTTACTAATCCACACTGAGCTCTCTGACCTGTGAGTGGGTTTAC 2883
3038 CGAGCAACCCGAAATGCAATTTTACAGAGTACACCTTAAAGTATGAGCAATTAACAG 3097
2884 CTACCACTCAATGATGTTTGTGATCATCATCATCTGAAAGTTTACCAATTAACACAC 2943
3098 CATGAATTTAGCCCTCTGTGATTTGAAATTTCTGCAACAAAGACAGGTGACTT 3157
2944 CATGAATTTAGCCCTCTGTGATTTGAAATTTCTGCAACAAAGACAGGTGACTT 3003
3158 TAAAAATTTAATTTACAGACTCGATATATGATTTATTTCTATGCAACAAATCAAGCAG 3217
3004 TAAAAATTTAATTTACAGCAACATCAAGTATCACTTATCAATCAACATCAAGTGG 3063
3218 GATCAAGAAATCAATTTACAGAGAAAGCACTAAGCTGTGATGAGTGTATTTCTTC 3277
3064 GATCAAGAAATCAATTTACAGAGAAAGCACTAAGCTGTGATGAGTGTATTTCTTC 3108
3278 CACTGATGTAGTGCAGGCAAGTTCAGAGCTGTAAATTAACAGATCAAGCAATCTTACG 3337
3109 -----AAGTCAACACCTTATTCAGAAAGATCAAGAAATGTTACAA 3147
3338 CTGCACTGCTGAGACTATGCAATTAATGTTGGAAATATGAGGACCAAGCATGTCGA 3397
3148 CAGCTGCTGCTGAGACTATGCAATTAATGTTGGAAATATGAGGACCAAGCATGTCGA 3207
3398 ACTTTATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3457
3208 ACTTTATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3267
3458 ATGTTCTTCGAGCTTCTTGTGGTTTAAAGGCTTATATCCAGAGAACAGATTAACAAATTC 3517
3268 ATGTTCTTCGAGCTTCTTGTGGTTTAAAGGCTTATATCCAGAGAACAGATTAACAAATTC 3327
3518 GAGTTGTGTGTGGGGAATCTGTGTTTGTGAGTTCAAGAGATGTTTGAACAAGCC 3577
3328 GAGTTGTGTGTGGGGAATCTGTGTTTGTGAGTTCAAGAGATGTTTGAACAAGCC 3387
3578 CAGGATGGAAGCCGAGAGGATGATTTGCAACTCAGGCGTGTTCATTTGCTGATGT 3637
3388 CAGGATGGAAGCCGAGAGGATGATTTGCAACTCAGGCGTGTTCATTTGCTGATGT 3447
3638 GTGCTGTGCTCTCTTATTTAATTTGCTGATTTGTTGCTTCAAGAAAGCAAG 3697
3448 GTGCTGTGCTCTCTTATTTAATTTGATTTGATTTGTTGCTTCAAGAAAGCAAG 3507
3698 GTGTTAATTTCACTTAAAGAAAGAAAGTCCCATGCTGACCTTGAATTCAGCCTA 3757
3508 GTGCAAAATTCCTAGTGAAGAAAGAAAGATGCAATGCTGATTCAGAAATTAAGCCTTA 3567

QY 3758 TGAAGAGATGATGAGACATTTGAGAAATACAGTATGACAGAGACCAAGCCCTTTGA 3817
 DB 3568 TGAAGAGATGATGAGACATTTGAGAAATACAGTATGAGAGACCAATAAACCTCTAA 3627
 QY 3818 AAAAGAGAGTGCACACTCTTTCAGACAGACGTGTGAAAAAGAGTATGTACAGACGC 3877
 DB 3628 AAAAGAGAGTGCAGACCGTCAGACAGACGTGTGAAAAAGAGTATGTATGATGTT 3687
 QY 3878 TAGTTACTATGAGAGAGGGGTATATGCGCAGTTCAATGAGATGAGTGCCTCTTATTTGAC 3937
 DB 3688 TAGTTACTATGAGAGAGGGGTATATGCGCAGTTCAATGAGATGAGTGCCTCTTATTTGAC 3747
 QY 3938 AATACAGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3997
 DB 3748 AATACAGCGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3807
 QY 3998 CTCCTGTCAAGCAGATGATTTCTTTGTTTATTTTAACTCAAGCCCAATTT 4051
 DB 3808 CTCCTGTCAAGCAGATGATTTCTTTGTTTATTTTAACTCAAGAGAGAGAGAGAGAG 3861

RESULT 8

AAZ38181
 ID AAZ38181 standard; DNA; 1371 BP.

AAZ38181;

14-FEB-2000 (first entry)

Human Nr-CAM gene fragment.

Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation;
 tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
 degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
 systemic lupus erythematosus; demyelinating disease; growth; human; ss.

Homo sapiens.

MO995380-A1.

04-NOV-1999.

27-APR-1999; 99MO-US009039.

27-APR-1998; 98US-0083152P.

14-DEC-1998; 98US-0112098P.

(PACT-) PACIFIC NORTHWEST CANCER FOUND.

Murphy GP, Boynton AL, Sehgal A;

WPI; 2000-023268/02.

Use of neuron-glia-related cell adhesion molecule for developing agents
 for the diagnosis and treatment of e.g. cancers, hyperproliferative
 disorders, growth deficiencies, degenerative disorders, trauma or wounds.

Example; Page 181-182; 183pp; English.

The invention relates to the use of neuron-glia-related cell adhesion
 molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
 preventing disorders involving cell proliferation. An antisense nucleic
 acid complementary to at least a portion of an RNA transcript of a Nr-CAM
 gene can be used to inhibit hyperproliferation of a tumor cell, for the
 treatment of tumorigenesis. Agents which inhibit and promote Nr-CAM
 function can be used for the treatment of various diseases and disorders
 (see AAZ38152 for a detailed description). The products can also be used
 for detection, diagnosis and production of animal models. The present
 sequence represents a human Nr-CAM gene fragment

Sequence 1371 BP; 438 A; 313 C; 281 G; 339 T; 0 U; 0 Other;

Query Match 33.2%; Score 1371; DB 3; Length 1371;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ATGCCGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 189
 DB 1 ATGCCGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 190 ATGATTAAGTGCACCTGGAAGTACCTCTGTATGATCCAAACTCTTGAAGACTGTGACAGCT 249
 DB 61 ATGATTAAGTGCACCTGGAAGTACCTCTGTATGATCCAAACTCTTGAAGACTGTGACAGCT 120
 QY 250 CCAACCATCACCACACAGCTCTCCAAAAGATTACATTATTTAGACCTTCGGAGAAATTTGTA 309
 DB 121 CCAACCATCACCACACAGCTCTCCAAAAGATTACATTATTTAGACCTTCGGAGAAATTTGTA 180
 QY 310 ATCCAGTGTGAAGCCAAAGGGGAAACCGCCCAAGCTTTCTGTGACCCGTATGGAGACT 369
 DB 181 ATCCAGTGTGAAGCCAAAGGGGAAACCGCCCAAGCTTTCTGTGACCCGTATGGAGACT 240
 QY 370 CATTTTGAATCATGATTAAGAGACCTCTGTGTCAACATGAAGCTTGACAGAAACGCTCATTA 429
 DB 241 CATTTTGAATCATGATTAAGAGACCTCTGTGTCAACATGAAGCTTGACAGAAACGCTCATTA 300
 QY 430 ATTAACATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489
 DB 301 ATTAACATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 490 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549
 DB 361 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 550 TTGTGAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
 DB 421 TTGTGAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 610 CCTCGAAGACCCCAATTGATTAACCAACCACTTAAATTTTGGATGATTAATTCCTTT 669
 DB 481 CCTCGAAGACCCCAATTGATTAACCAACCACTTAAATTTTGGATGATTAATTCCTTT 540
 QY 670 CAAAGAGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 DB 541 CAAAGAGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 730 AATGTCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
 DB 601 AATGTCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 790 CAAACCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
 DB 661 CAAACCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 850 GACACATTAAGCTTAATTTGAGTACCTGAGTGTATTTAGGCTTAATCAAGTAGAGAG 909
 DB 721 GACACATTAAGCTTAATTTGAGTACCTGAGTGTATTTAGGCTTAATCAAGTAGAGAG 780
 QY 910 AGGCCACCAACATTTTAACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969
 DB 781 AGGCCACCAACATTTTAACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 970 AATGTCCTTCACTGAGAGTCACTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
 DB 841 AATGTCCTTCACTGAGAGTCACTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 1030 AAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1089
 DB 901 AAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 1090 CAGATCATTCATGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149
 DB 961 CAGATCATTCATGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 1150 TTAGAGAGCATCACCATTAATTTCTGTAGAGTTAAAGCGGCTCATCTGATGATCA 1209

Db 1021 TTAGAGCCATCCACCATTCATTTCTGTAGATTAAAGCGCTCCATCTGATCACA 1080
 QY 1210 GCCCCTCAAAATCTTGCTGTCCAGAGAGATGGAGCTTGATCTGACAGCTAAT 1269
 Db 1081 GCCCTCAAAATCTTGCTGTCCAGAGAGATGGAGCTTGATCTGACAGCTAAT 1140
 QY 1270 GGCACACCCCAACCCAGAAATAGCTGTGTACAAATGAGTCCCAATACAAATTCGCCCT 1329
 Db 1141 GGCACACCCCAACCCAGAAATAGCTGTGTACAAATGAGTCCCAATACAAATTCGCCCT 1200
 QY 1330 GATGACCCCAAGCAAAATAGATGCGCATACCATTTATTTTCAATGTTCAAGAAAGA 1389
 Db 1201 GATGACCCCAAGCAAAATAGATGCGCATACCATTTATTTTCAATGTTCAAGAAAGA 1260
 QY 1390 TCAAGTGCAGTATATCAATGCAATGCTCTAATGATATGATTTACTGGCAACGCA 1449
 Db 1261 TCAAGTGCAGTATATCAATGCAATGCTCTAATGATATGATTTACTGGCAACGCA 1320
 QY 1450 TTTGTAAATGCTGCTGAGTGCACACCAAGATCTCTACACCTGCAAAACACA 1500
 Db 1321 TTTGTAAATGCTGCTGAGTGCACACCAAGATCTCTACACCTGCAAAACACA 1371

RESULT 9

AAZ38182 standard; DNA; 1371 BP.

AAZ38182;

14-FEB-2000 (first entry)

Rat Nr-CAM gene fragment.

Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation;
 tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
 degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
 systemic lupus erythematosus; demyelinating disease; growth; rat; ss.
 Rattus norvegicus.

W09955380-A1.

04-NOV-1999.

27-APR-1999; 99WO-US009039.

27-APR-1998; 98US-0083152P.

14-DEC-1998; 98US-0112098P.

(PACI-) PACIFIC NORTHWEST CANCER FOUND.

Murphy GP, Boynton AL, Sehgal A;

WPI, 2000-023268/02.

Use of neuron-glia-related cell adhesion molecule for developing agents
 for the diagnosis and treatment of e.g. cancers, hyperproliferative
 disorders, growth deficiencies, degenerative disorders, trauma or wounds.
 Example: Page 182-183; 183p; English.

The invention relates to the use of neuron-glia-related cell adhesion
 molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
 preventing disorders involving cell proliferation. An antisense nucleic
 acid complementary to at least a portion of an RNA transcript of a Nr-CAM
 gene can be used to inhibit hyperproliferation of a tumor cell, for the
 treatment of tumorigenesis. Agents which inhibit and promote Nr-CAM
 function can be used for the treatment of various diseases and disorders
 (see AAZ38182 for a detailed description). The products can also be used
 for detection, diagnosis and production of animal models. The present
 sequence represents a rat Nr-CAM gene fragment

Sequence 1371 BP; 403 A; 339 C; 291 G; 338 T; 0 U; 0 Other;

Query Match 26.4%; Score 1092.6; DB 3; Length 1371;
 Best Local Similarity 87.3%; Pred. No. 1.9e-311;
 Matches 1197; Conservative 0; Mismatches 174; Indels 0; Gaps 0.

QY 130 ATGCCGAAAAGAAAGCGCTTAATCTGCGGAGAGTGCCTTGATTTCTTCTGTCGAG 189
 Db 1 ATGCCGAAAAGAAAGCGCTTGCTGTCGAGAGAGCGCCCTGTCTTCTGTCGAG 60
 QY 190 ATGATTAATGCACTGGAAGTACCTCTGATCCAAACCTTCTGGAAGTCTGACAGCT 249
 Db 61 ATGATCAAGCGCTGGAAGTCTCTTGTATCCAAAGCTCTTGATGACCTGATACGCT 120
 QY 250 CCAACCATACCCCAACAGCTCTCAAAAAGATTACATTTATGACCTCGGAGAAATTTGTA 309
 Db 121 CCAACTATACCTCAACAGCTACCAAAAAGATTCATGATGACCTGAGAGAAATTTGTA 180
 QY 310 ATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTGTGACCCGTAATGGACT 369
 Db 181 ATCCAAATGTGAGGCCAAAGGAAACCTCTCAAGCTTTTCTGTGACCTGTAACGGAACA 240
 QY 370 CATTTGACATCGATTAAGAACCTCTGTGTACATGAAAGCTTGCGACAGAAACGTCATA 429
 Db 241 CATTTGACATGACAAAGAACCTCTGTGTACTATGAAGCTTGCGACAGAAACCTGTGTC 300
 QY 430 ATTAACATCATGAGCGAAAGGAAAGCTGAGACTATGAAGAGTCTATCAGTACAGCA 489
 Db 301 ATCAACATCATGATGAGAAAGGAAAGCGAGACCTATGAAAGGGTTTACAGTACAGCA 360
 QY 490 AGGAACGAAGCGGAGCTGCAAGTCTTAATAACATTTGTCGCGCCATCCAGATCACCA 549
 Db 361 AGGAATGAGCGCGGAGCTGTCTGTCAATAACATTTGTCGCGCCCTTAAAGTCAACC 420
 QY 550 TTGTGACCAAGAAAGAAACCTTGAAACATCACTTCAAGTGTCACTTTAGTACTT 609
 Db 421 TTGTGACCAAGAAAGAAACCTTGAAACATTAATCTCCAGATGTGCTACTGTACTA 480
 QY 610 CCTGACAGACCCCAATTTGATTAACACACCTTAATATTTTGGATGATTAATCTCTT 669
 Db 481 CCAATGTAGGCTCCCAATTTGATTAACACCGGCAATTAATTTTGGATGATTAATCTCTT 540
 QY 670 CAAGAATCTTCCAAAGTGAAGAGTCTCTCAAGTGTGAATGGGACCTTTATTTTTC 729
 Db 541 CAAGAATCTTCCAAAGTGAAGAGTCTCTCCAAAGTGAATGGGACCTTTTACTTCTCC 600
 QY 730 AATGCTCTCCCAAGAGACACCGGAGACTATATCTGTATGCTAATTTATATATCT 789
 Db 601 AATGCTCTCCCAAGAGACACCGGAGACTATATCTGTATGCTAATTTATATCACT 660
 QY 790 CAACCATACAGCAAGAGCACTATTCTGTGAAGGTATTTAGTGAATGAATGAAT 849
 Db 661 CAACCATACAGCAAGAGCACTATTCTGTGAAGGTATTTAGTGAATGAATGAAT 720
 QY 850 GACACTATAGCTGTCAATTTAGTGAACACTGATGTTTATGCTGAATCAAGTAGAGAG 909
 Db 721 GACACTATAGCTGTCAATTTAGTGAACACTGATGTTTATGCTGAATCAAGTAGAGAG 780
 QY 910 AGGCCACCAACATTTTAACTTCCAGAGGCAATGCAATGAACAAAGAGAAATTAAGAGA 969
 Db 781 AGGCCACCAACATTTTAACTTCCAGAGGCAATGCAATGAACAAAGAGAAATTAAGAGA 840
 QY 970 AATGCTTTTACAGTGAAGTGAATGCAAGAGACTGCTTACCCCAATTTATTTCTGGGCA 1029
 Db 841 AATGCTTTTACAGTGAAGTGAATGCAAGAGACTGCTTACCCCAATTTATTTCTGGGCA 900
 QY 1030 AAGGAAGATGGAATGCTTACCCCAAGAGCAAGTGTATTAAGAACTTTGAGAAACCTTGG 1089
 Db 901 AAGGAAGATGGAATGCTTACCCCAAGAGCAAGTGTATTAAGAACTTTGAGAAACCTTGG 960
 QY 1090 CAGATCATTAATGTTTCAAGAGCAAGTGTGAAATTTACCAATGATATGCAAAATGCA 1149
 Db 961 CAGATCATTAATGTTTCAAGAGCAAGTGTGAAATTTATCAGTCAATGCAAAATGCA 1020

QY 1150 TTAGAGCCATCCACCATCATTTCTGTAGATTAAGCGGCTCCATCTGATCACA 1209
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 Db 1021 TTGGAGCGCGTCCATCATTCATTTCTGTACAGTTAAAGCGGCTCCCTACTGAGATTGT 1080
 |||||
 QY 1210 GCCCTTCAAAATTTTGTCTGTCTCCCAAGAGAGATGGAGCCTTGATCTGCAGAGCTAAT 1269
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 Db 1081 GCACCTTCACAACTCCGTCTTCTCCCAAGAGAGATGGAGCCTCATCTGCAGAGCTAATC 1140
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 QY 1270 GGCACCCCAAAACCCAGAAATTTAGCTGTTTAACAATGGAGTCCCATAGAAATTTGCCCT 1329
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 Db 1141 GGCACCCCAAAACCCAGAAATTTAGCTGTTTAACAATGGAGTCCCATAGAAATTTGCTCTC 1200
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 QY 1330 GATGACCCAGAGAAAATAGATGCGATACCATTAATTTTCAATGTTCAAGAAAGA 1389
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 Db 1201 GATGACCCAGAGAAAATAGATGCGATACCATTAATGTTTCAATGTTCAAGAAAGC 1260
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 QY 1390 TCAAGTGCAGTATATAGTGCATATGCTCTTAATGATATGATATTTACTGGCAAAACGA 1449
 |||||
 Db 1261 TCAGTGCAGTATATAGTGCATATGCTCTTAATGATATGATATTTACTGGCAAAATYGA 1320
 |||||
 QY 1450 TTTGTAAATGTGCTGAGCGACGACGAAATCTGACACCTGCAACCA 1500
 |||||
 Db 1321 TTTGTAAATGTGCTGAGCGACGACGAAATCTGACACCTGCAACCA 1371
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RESULT 10
 AAD49596
 ID AAD49596 standard; cDNA; 4360 BP.
 AC AAD49596;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE Human cytoskeleton-associated protein, CSAP-7 cDNA.
 XX
 KW Human; cytoskeleton-associated protein; CSAP-7; atherosclerosis; cancer;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 276..4355
 FT /*tag= a
 FT /product= "Human CSAP-7"
 FT sig_peptide
 FT 276..353
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 FT sig_peptide
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 FT 354..4352
 FT /*tag= e
 FT /product= "Human mature CSAP-7 protein"
 FT
 PN WO200279404-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 25-MAR-2002; 2002WO-US009288.
 XX
 PR 29-MAR-2001; 2001US-0280508P.
 PR 03-APR-2001; 2001US-028123P.
 PR 13-APR-2001; 2001US-0283769P.
 PR 04-MAY-2001; 2001US-028609P.
 PR 10-MAY-2001; 2001US-0290518P.
 PR 18-MAY-2001; 2001US-0291870P.
 PR 29-MAY-2001; 2001US-0294451P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Hafalia AJA, Tang TY, Yue H, Khan FA, Ison CH, Baughn MR,
 PI Warren BA, Dugan BM, Thangavelu K, Honchell CD, Azimzai Y;

PI Elliott VS, Burford N, Ding L, Yue H, Becha S, Emerling BM;
 PI Richardson TW, Lee SY, Bandman O, Lai PG, Lee S, Gietzen KJ;
 PI Walia NK, Griffin JN, Lee EA, Swarnaker A, Ring HZ, Jones KA;
 XX
 DR MPI: 2003-092894/08.
 DR P-PSDB; AAE32109.
 PT New human cytoskeleton-associated proteins, useful for preparing a
 PT composition for diagnosing or treating a disease or condition associated
 PT with decreased expression or overexpression of functional CSAP e.g.,
 PT cancer.
 XX
 PS Claim 5; Page 210-211; 233pp; English.
 CC The invention relates to new human cytoskeleton-associated protein (CSAP)
 CC and its polynucleotide. The polypeptide is useful for preparing a
 CC composition for diagnosing or treating a disease or condition associated
 CC with decreased expression or overexpression of functional CSAP e.g.,
 CC atherosclerosis or cancer. The present sequence is human CSAP-7 cDNA. The
 CC invention is useful in gene therapy
 XX

SQ Sequence 4360 BP; 1067 A; 1321 C; 1185 G; 787 T; 0 U; 0 Other;

Query Match 18.9%; Score 779.8; DB 7; Length 4360;

Best Local Similarity 54.6%; Pred. No. 1.1e-218;

Matches 1701; Conservative 0; Mismatches 1387; Indels 29; Gaps 6;

QY 167 CCCTGATTCCTCTCCCTGCGCAGATGATTAAGCACTGGAAGTACCTGTGTCGAAC 226
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 Db 313 CCTTCCTCTCTGCTCCTCCTCCTGCTTGGCGAGCATGGAATTTCTTATGATTCAGCA 372
 |||||
 QY 227 TTTCTGAAGACTGTGTAGAGCTCCACCATCACCCACAGTCTCCAAAGATTACATTA 286
 |||||
 Db 373 TTCAGAAAGAGCTGACGACGCGCCACCATCACAGTCAAGAGATGATCAG 432
 |||||
 QY 287 TTGACCTCTGGGAGAAATTTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCT 346
 |||||
 Db 433 TGGACCCCGTGATTAACATCTGATTTGAGTGAAGCAAAAGGAAACCTGCCCCAGCT 492
 |||||
 QY 347 TTTCTGAGACCGGTATGGAAGCTCATTTTGCATGATTAAGAACCTGTCGATCATGA 406
 |||||
 Db 493 TCCACTGACACGAAACAGACGATTTCTTCAATGATCCCAAGAACCCCGGGTGTCAATGA 552
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 QY 407 AGCTTGACACGAAACGCTCATTAATTAATCATGATGAGGAAGGAAAGTGAAGCTATG 466
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 Db 553 GAGAGAGCTGTGAGACCTGTGTGATTAATCTCGAGTGGGGGGCGGCGAGAGATATG 612
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 QY 467 AAGAGTCTATCAGTGTACAGCAAGAAAGAAAGCGGAGCTGCACTTTCTAATAATTC 526
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 Db 613 AAGGAGAAATATCAGTGTGCGCCGCAAAATTTGGCAAGCGCCCTGTCAATAGATTC 672
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 QY 527 TTGTCGGCCCATCCAGATCAACATGTTGGAGCCAAAGAAACTTGAACCAATCACACTTC 586
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 Db 673 GCTTCAGGTGTCTAATATCTCTGTGTGCCCAAGAAACCTTAAGCCTGTGTGTGTC 732
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 QY 587 AAGAGTGTAGTCTTTAGTACTTCCCTGAGACCCCAATTTGATTAACACCACTTAATA 646
 |||||
 Db 733 AAGAGGGGCTCCTTTGAAGCTCCAGTGAACCCCGCGCTGGAATTCATCCCGGTCA 792
 |||||
 QY 647 TATTTTGTAGTATTAATCTTTCAAAAGACTTCACAAAGTGAAGAGTTTCTCAAGTT 706
 |||||
 Db 793 TCTTCTGATGAGCAGCTTCATGAGAGCCATCACCAAGACAAAGTGTCTCTCAGGGCC 852
 |||||
 QY 707 TGAATGGGACCTTATTTTCCATGTCTCCAGAGAGACACCGGAGAGCTATATCT 766
 |||||
 Db 853 ATTAAGGAGACCTTAATCTTCAAGAGTGTGAGAGACGACCGATCACTACATT 912
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 QY 767 GTTATGCTAGATTATATCACTCAAAACATACAGAGAGCACTTATTTCTGTGAAG 826
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 Db 913 GTTAAGCCCGCTTCACTTCAACCCACATCCAGAGAGAAACCTTTCAACCCCAAG 972
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 QY 827 TGATTCAGTGATGAATGAATGAACACTATAGCTGTAATTTGATGAAGTCACTGAGTTT 886
 |||||

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Db 973 TCCCTACCAACCACTTAAATGAC-----TCGTCCTTAAGAAAACAACCTGACATGT 1026
Qy 887 ATGTGCTAAATCAAGTAGAGAGGCAACAACTTTTAACTCCAGAGCAATGCA 946
Db 1027 AAGGTGCCCCGAGAGATTGCAAGAAAGAACACAGCTTCATGATCCCGAGGCAACGCGCA 1086
Qy 947 GTAACAAAGAGAAATTAGAGAAATGTGCTTCACTGAGTGATGAGAGAGATCG 1006
Db 1087 GGAGCCAGATGGTCTCGTGGCATGGACCTCGCTGGAAATGCAATGCTCCGAGGATC 1146
Qy 1007 CTACCCCAATTATTACTGGGCAAGAGAAAGATGGAATGCTACCCAAAACAGACATTT 1066
Db 1147 CAACACCAACATCGCATGTATCAAGAAAGTGGGAGACCTCCATCTGATTAAGGCCAAGT 1206
Qy 1067 ATPAGAACTTTGAGAAACCTTGACATGATTCATGTTTCAAGAGAGACTCGGAATT 1126
Db 1207 TTGAGAACTTTAATAGGCCCTGCGTATCAAAATGCTCTGAGAGAACTCCGAGGAGT 1266
Qy 1127 ACCAATGTATAGCAAAAAATGCAATTAGAGCCATCCACATACCATTTCTGTAGATTA 1186
Db 1267 ATTTGCGCTGGCTCCAAACAGATGGGAGAGATCCGGGACAGATCTGGTGAAGATTA 1326
Qy 1187 AAGCGCTCCATPCTGATGACAGCCCTCAAAATCTTGCTGTCCTCCAGAGAGATG 1246
Db 1327 AAGGCTGCTCCCTAAGCTGGAAGAGAACCAAGAACTTATCTGCTGCTGGAGAGATG 1386
Qy 1247 GAGACCTGATCTGAGAGCTAATGAGCAAGCCCAACCCAGAAATTAGCTGTTAAACAATG 1306
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Db 1986 ACCGTCTCGTGGCTGAAGATGACAGCCGCTCTATATTGGAACAGAGATGAAGAGAA 2045
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Oy 3091 AACAGACATGATTAATTAAGCCCTCTGTGATATTGAAAAATTCCTGCCAAGACACGG 3150
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Oy 3151 TGGACCTTAAAAATTTAAATTTACACACTCCATATTAAGTTTATTTATGACAAACA 3210
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Db 3300 TTCACGGTCCAAAGAACGAGCCCGGTGTACCGCTTACCGCTTACCGCCGACGAGCG 3359
Oy 3211 TCAGCAGATCAAGAGTCAAAATTAACAGAGAGAGTAAACAATGTGATGAAGCT 3267
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RESULT 11
AAD49595
ID AAD49595 standard; cDNA; 4080 BP.
AC AAD49595;
XX
XX 24-MAR-2003 (first entry)
DE Human cytoskeleton-associated protein, CSAP-6 cDNA.
XX
XX Human; cytoskeleton-associated protein; CSAP-6; atherosclerosis; cancer;
KM gene therapy; gene; 88.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
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    /tag= b
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XX WO200279404-A2.
XX
XX 10-OCT-2002.
XX
XX 25-MAR-2002; 2002MO-US009288.
XX
XX 29-MAR-2001; 2001US-0280508P.
XX 03-APR-2001; 2001US-0281323P.
XX 13-APR-2001; 2001US-0283769P.
XX 04-MAY-2001; 2001US-0286009P.
XX 10-MAY-2001; 2001US-0290518P.
XX 18-MAY-2001; 2001US-0291870P.
XX 29-MAY-2001; 2001US-0294451P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Hafalia AJA, Tang TY, Yue H, Khan FA, Ison CH, Baughn MR,
PI Warren BA, Duggan BM, Thangavelu K, Honchelli CD, Azimzai Y,
PI Elliott VS, Burford N, Ding L, Yue H, Becha S, Emerling BM,
PI Richardson TW, Lee SY, Bandman O, Lai PG, Lee S, Gietzen KU,
XX Walla NK, Griffin JA, Lee EA, Swarnakar A, Ring HZ, Jones KA,
DR WPI, 2003-092894/08.
XX P-PSDB; AAB32108.
XX
XX New human cytoskeleton-associated proteins, useful for preparing a

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PT composition for diagnosing or treating a disease or condition associated
PT with decreased expression or overexpression of functional CSAP e.g.,
PT cancer.
PS Claim 5; Page 209-210; 233pp; English.
XX
XX The invention relates to new human cytoskeleton-associated protein (CSAP)
XX and its polynucleotide. The polypeptide is useful for preparing a
XX composition for diagnosing or treating a disease or condition associated
XX with decreased expression or overexpression of functional CSAP e.g.,
XX atherosclerosis or cancer. The present sequence is human CSAP-6 cDNA. The
XX invention is useful in gene therapy
SQ Sequence 4080 BP; 987 A; 1241 C; 1117 G; 735 T; 0 U; 0 Other;

Query Match 18.8%; Score 778.2; DB 7; Length 4080;
Best Local Similarity 54.5%; Pred. No. 3,2e-218;
Matches 1700; Conservative 0; Mismatches 1388; Indels 29; Gaps 6;

Oy 167 CCTGATTTCTTCTCTGTCGACGATGATTAAGTACCTGTAATCCAAAC 226
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Oy 227 TTTTGAAAGCTTGTGTAAGCTTCCATCAGTCCAAACAGTCTTCAAAAGTTACATTA 286
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Oy 287 TTGACCTTCGGAGAGATATTTGAATCCAGTGGAGCCAAAGGAAACCGCCCAAGCT 346
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Db 973 TCTTCAACCAACACCTTATTAATGAC-----TGCTCTTAAGAAACACCTTGACATGT 1026
Oy 887 ATGAGTCTAATCAAGTAGAGAGAGCCCAACAATTTTAACTCCAGAGCAATGCA 946
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Db 1027 ACAAGTCCCGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
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Oy 947 GTAACAAAGAGAAATTAAGAGAGAAATGTGCTTCACTGAGATGATGAGAGAGAGAGAGAG 1006
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Db 1087 GCAGCCAGATGCTGCTTGTGCGATGAGACCTCTGCTGGAATGATGCGCTCCGGGGTCC 1146
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 Qy 1427 ATGATATTTAATGCAAAAGCATTTGTAATGTGCTGAGCCAGCAGCAATCTCA 1486
 Db 1301 ATGCTACTGCTGAGCAAGCTTTGTGATGTGTGATGTGCTGCTCGATCTGT 1360
 Qy 1487 CACTGCAACACACTCTACAGGTCAATGCAACAGGCTGTTTACTAGACTGTGCT 1546
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 Db 1660 AAGAGGGGACACCGTGCATCTGAGATGTGGGTGAAGACAGACCCCTCTGAAGCT 1719
 Qy 1846 ACTGTCTGTGTGTAAGACAAACAGGAACTGCCCATGATGAAGATGACTCTTAC 1905
 Db 1720 ACCGTCTACTGTGAAGATGACAGCGCTTATATTTGAAGAAAGATGAAGAA 1779
 Qy 1906 AAGATCATCTAGTGTAGTGTAGTCACTGATGATGATGATGATGATGATGATGAT 1965
 Db 1780 GAGCACTCCCTGACATCTTTGGGTGACAGAGCGGACAGAGGAGATTAACGCTGTCT 1839
 Qy 1966 GCGAACACCACTCTGAGACGCTCTCCGACAGCTGTGTGTTAGCTTGTCTTACT 2025
 Db 1840 GCGAGCACCGAGCTAGACCAAGACTGGCCCAAGGCTTACCTGCTAGAGAGG--- 1896
 Qy 2026 CCAACTCAGCTCCGTTTACATGTCCCAATCTCTCCCTTGAATCTTGAATCTGACAT 2085
 Db 1897 -----CGAGCTGGCCCGGACCTGAGCTGACGAGC 1929
 Qy 2086 CAATTTGACAAAGTTCAGCTGTATGAGACCCAGGAGATGACAAATGACCCCAT 2145
 Db 1930 CTGCGCGAGAGAGCTGTGCTGCTGATCTGATCCCCGGGATGTAACAGCCCATC 1989
 Qy 2146 ACMAATTCATCATGAAATATGAAATGCAATGCAAGCAAGGCTGTGACCAACCA 2205
 Db 1990 ACAGACTAGCTGTCACTTTGAAGAAAGCAAGTTCCAACTGGGCTCTGAGATGACAT 2049
 Qy 2206 ACTGAATTTCTGGAACACAGACACAGCCCACTGAAGCTGTCTCTTAAGTGAATAC 2265
 Db 2050 TCCAAATACCCCGAGAGGTTAACTACAGCTGCTCCGCTGTCTCCGTATGTCAATAC 2109
 Qy 2266 TCTTTCCGCTGATGAGAGTGAACAGATGAGGAAAGACTTGGCCAGAGGAGCTGTG 2325
 Db 2110 CAGTTCCTGTCTATGCTCAACAGAGTTGAGAGACACCAACCTGCTCCATCTGAG 2169
 Qy 2326 CAGTATTTGAGAAAGCTCTGAGAACCAAGATTAACCCCAAGCTGTGGAAGAGTGA 2385
 Db 2170 CGCTACGAGACAGAGAGACACCCCGAGATCAATCTGAGATGTAAGAGGAGAGGG 2229
 Qy 2386 TCAAGCTGATTAATTTGAGATTAAGTGAAGCTTGAATGTTGAATCTTAATGAG 2445
 Db 2230 ACCAGAAAGAACCAATGAGATCACTGTGAGACGCTCATGAAATGCCACTCTTGTGC 2289
 Qy 2446 CAGGCTTCACTGATCAAAAGTTAGCTGAGCCAGAAAGATGATGAATGACATCT 2505
 Db 2230 CCAACCTGCTTCAATTTGTCAAGTGAAGGAGAGAGATCTGAGAGGCTTGAAGAAC 2349
 Qy 2506 GTGTGTGTGAGAAATGATCAAAATATATTTCTCAGGACAGCCCACTTTGTTCCATAC 2565
 Db 2350 GTCAAGTGTG---GGCTCTGCTAGTGTGTGGGAGAGACCCAGATCTAGGTGCTAT 2406
 Qy 2566 CTGATCAAAAGTTCAAGCCCTGATGATGATGAGGTTTGTCCCGAGCTGATGATG 2625
 Db 2407 GAGATCCAGTCCAGGCTGAAGAAATGATCTTGGGAAAGGCTGAGCTGAGTCTCATC 2466
 Qy 2626 GGAATCTTGGAGAAAGCTGCCAAATGAGTGTCTCTGGAAGCTGCTGTGATGATGAGT 2685
 Db 2467 GTTACTCCGAGAAAGATTAATCCAGGCTGTGAGCCCACTGAAGTTAAAGTCCAGTCTATG 2526
 Qy 2686 AACAGTACTTATAGCCAGAGTGTGAGACCAAGTACTCTGAAAGAGATCCAGAGAC 2745
 Db 2527 AACAGCAAGCATAGCTTCAAGTGAACCGGCTTACTCTGACAGCTCAGAGGACAG 2586
 Qy 2746 CTACAGGCTATGAGATTTACTATTGGAAGACCAAGATTCATCTTAAAGAAACAGAGCT 2805
 Db 2587 CTCAAGAGATACCGAGCTACTACTGAGGAGAGAGAGCTTGTGAAGAAACCTGTGGTGTG 2646

QY 962 TAAAGAAATGTCTTTCACGTGAGTCAATTCAGAGAGACTGCCATACCCCAATTAATTT 1021
DB 670 TTGTTGGCATGAGCTTCCTGCTGGAATGATGCGCTCCGGGGTCCCAAGACAGAGACTCG 729
QY 1022 ACTGGCAAGAGAAAGTGAATGCTACCCAAAACAGAGACATTTATAGACCTTTGAGA 1081
DB 730 CATGTACAGAAAGGTGGGAGCTCCCATCTGATTAAGCCAAAGTTTGAGAACCTTTAATA 789
QY 1082 AAACCTGACATCTTCAATGTTTCAAGACAGACTGTGAATTAATCAATGATAGCA 1141
DB 790 AGGCCCCGTATACAAATGTCTGAGAGAACTCCGGGAGTATTTCTGCTGGCT 849
QY 1142 AAATGATTAAGAGCCATCCACCATACATTTCTGTTAAGTAAAGCGGCTCCATCT 1201
DB 850 CCAACAAAGTGGGAGAGTCCGGACACAGATCTCGGTGAGATGAAGGTGCTCCCTACT 909
QY 1202 GATTCACAGCCCTCAAAATCTTGTGTGTCCCAAGAGAGATGGGACCTTGATCTGCA 1261
DB 910 GGCTGACGAACCAAGAACCTTATCTGGCTCTGGCGAGATGGGAGACTGGTGTGTC 969
QY 1262 GAGCTATGCAACCCCAAAACCCAGAAATTAAGTGTGTTAACAAATGAGTCCCAATGAAA 1321
DB 970 GAGCCATGGAACCCCAAAACCCACTGTCCAGTGAATGTGAATGGGAACTTTGCAAT 1029
QY 1322 TTGCCCTGATGACCCCAAGAAAATAGATGGCATACCATTTATTTTCAAAATGTTT 1381
DB 1030 CGGCACACCTTAACCCAAACCGTGAAGTGGCGGAGACACATCACTTCCGGGACACCC 1089
QY 1382 AAGAAAGATCAAGTGAATATCAATGATGCAATGCTTAAATGAATATTTAATCTGG 1441
DB 1090 AGATCAGACAGAGGCTGTGTATCCAGTGAACACTTCAACGAGATGGCTACTCTGTGG 1149
QY 1442 CAAAGCATTTGTAATGTGTGTGTGTGAGGACCAAGAACTTCAACCTGCAAAACAC 1501
DB 1150 CCAAGCCCTTTGTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1209
QY 1502 TCTACAGGTCAATGCAACAGGCTGTCTTCTAAGACTGTGCTTCTTTGGTGTCTCTC 1561
DB 1210 TCAATGATGATTTCTTTACACCGGACGGGCTGAGCTGCTCTTTCTTTGGTGTCTCCA 1269
QY 1562 TCCCAACATCGATGTTTAAAGAGCTAAAGAAAGTGTCTTCAATGAATATTTATG 1621
DB 1270 TCCCAACATCGATGTTTAAAGAGCTAAAGAAAGTGTCTTCAATGAATATTTATG 1329
QY 1622 TTTTACATGAATGAATCTTTGGAATCAAGATCTTACATGATGCTTTAAAGAAATTC 1681
DB 1330 ATGTTTATGAAACGCGAGCTGGAAT-TAAGATATCCGCAAAAGGACCAAGGCTATC 1388
QY 1682 CTGTGCGCAAAAGACATGACGAATTAATCGTGTGTGCAAGAAATTAATTTAGGA 1741
DB 1389 TACACTGTGTGTGCGCAACATCTGTGGCAAAAGCTGAAAAACAAATCTCGCTGTGAGTTC 1448
QY 1742 TGGCAAAAGATGAATGTT-ACCTTACAGCCGGAATATGAGTTGTGCAAAAGAGGACATG 1800
DB 1449 AAAGACCCACAGAGATCTACCGGATGCCGAGGACCAAGTGGCCAGAAAGGGGACCAAG 1508
QY 1801 GTGTCTTTGAATGCAAGTGAATCACTTAATCCCTCACTGTCTGTGGCTG 1860
DB 1509 GTGCAAGCTGAGTGTGGGTGAAGACAGCCCTCCCTGAACCTCACTCTCTGTGGCTG 1568
QY 1861 AAGGACAAAGGAACTGCGCAAGTGAAGGTTCACTGTGCAAGAGATCATCTAAGTG 1920
DB 1569 AAGGATGAAGAGCCCTTATATTTGAAACAGATGAAGAGAGAGACGATTTCTGTACC 1628
QY 1921 GTAGCTGATGTCAATGACATGACAGCGGAGCTTACAGTGTGTGCGCAACCACTGTG 1980
DB 1629 ATCTTTGGGTGGAGAGAGGAGGACAGGGAAGTTTACAGTGTGTGCGCAACCAAGCTTA 1688
QY 1981 GACAGGTCTCGCCAGCGCTGTGCTTGAAGCTTTGTGCTCTCACTCAAGTCTCC 2040
DB 1689 GACCAAGACTGCGCAAGGCTTACCTCACTGCTGATGATCAAGGCTCACTCAACTAAC 1748

QY 2041 GTTTACGATGTC-----CCAAATCTCTCCCTTGACTTGAAGTACAGAT 2085
DB 1749 CGTTTGGCTGCCCTGCCAAAGAGCGCCAGACCGGCGCCCGGAGCTTGAGCTGACCGAC 1808
QY 2086 CAATTTGAAGAAAGTGTCACTGTCTATGAGACCCAGGCGGATGACAACTATGCCCATTT 2145
DB 1809 CTGGCCGAGAGGCTGTGGGTGAGCTTGATCTCCCGGAGATGCTTAACAAACAGCCCATTC 1868
QY 2146 ACAAAATCATCATGATATGAAATGCAATGACCAAGCCAGGCGTGGGACCAACCA 2205
DB 1869 ACAGACTAGTGTCTCAAGTTTGAAGAACAGTTTCAACTGGGGCTGGGATGACAT 1928
QY 2206 ACTGAAGTTTCTGGAACACAGACCAAGCCAGCTGAGCTGTCTTCTTACGTAATCA 2265
DB 1929 TCCAACTACCCCGGACGCTTAACTAGCGCTGTCTCCGGCTGTCCCGATGTCACTAC 1988
QY 2266 TCCCTTCCGCTGATGAGTGAACAGATTTGGAGAGCTTGGCCAGGAGCGTGTGAG 2325
DB 1989 CAGTTCCTGTGATTCATTCACAGAGTTGGGAGACGACCCAGCTCCCATCCGAG 2048
QY 2326 CAGTATTTGACGAAAGCCCTCAGAACAGATTAATAAACCCCAAGCTGTGGAAGACTGGGA 2385
DB 2049 CGCTACCGAACAGTGAAGACCCCGAGTCCAAATCTGTGAAGTGAAGAGAGGAG 2108
QY 2386 TCAGAGCTGATTAATTTGAGATTAAGTGAAGCCCTTGATGATTTTCAATCTAATGAG 2445
DB 2109 ACCAGAAAGAACATGAGATCACTGTGAAGCCCATTAATGCCACTTGGCTTTGGC 2168
QY 2446 CAGGCTTCAATCAAAAGTTAGCTGGCGCCAGAAAGATGTGATGATGATGATCT 2505
DB 2169 CCAACTGCTGCTCACTGTCAAGTGAAGGCGGAGAGACCTGAGAGGCTGGAACAAC 2228
QY 2506 GTGTGTGGCAATATTAATTAATATATGTCTAGGACCCCAACTTTTCCATAC 2565
DB 2229 GTCAAGTG--TGAGGCTCTGCTACGTGTGTGGGACAGCCCAAGTCAAGTGTCTAT 2285
QY 2566 CTGATCAAAAGTTCAAGGCTCTGATGACATGAGGTTTGGCCCGGAGCGAGCTGTAGCATG 2625
DB 2286 GAGATTCGAGTCAAGCTGAAATATGCTTGGGAAAGGCTCTGAGCGAGATCCGCTATC 2345
QY 2626 GGAATTTGGAAGAACCTCCCAATGTGTGCTCTGGGAGCGTGTGTGATGTGTG 2685
DB 2346 GGTACTCCGAGGAAGATTAATCCAGGGCTGGGCCCACTGAAGTTAAAGTCCGAGTCATG 2405
QY 2686 AACGATCTTATGCGGAGTGAAGTGTGAGACCCAGTACCTTGAAGAAAGATCCGAGGAC 2745
DB 2406 AACGACAGCCATCAGCTTCAAGTGAACCGGCTTACTCGACACGCTCAGGCGCAG 2465
QY 2746 CTACAAGCTATCGGATTTACTAATTTGAAGACCCAGAGTTCATCTTAAGAAACAGACGT 2805
DB 2466 CTCAGAGATACAGAGCTTACTACTGAGGAGAGAGAGAGCTTCTGAAGAACTGTGGTGT 2525
QY 2806 CACTTGAAGAAAGATCTCTCACTTCCAGGCGAGACAGATCAATGAGTGTGCGGGG 2865
DB 2526 TCTCAAGAGAGACAGAGAGCAGCTTCCCTGTGACCGCTCTCGTGGGTGTGTCCGCG 2585
QY 2866 CTAGAGCCCTTTAGCACTACACTGAATGTCCAGTGTGTAATGGGAAAGGAGGCGC 2925
DB 2586 CTCTTCCCTTACAGTACATCAAGCTGAGAGTGTGTGTGTGAATGGGAGAGTATGAG 2645
QY 2926 CAGGCGAGCCCTGACAGAGTCTTAAATCTCCAGAGAGAGTCCCGAGTGTCTCGTCT 2985
DB 2646 CTTGCGAGTGAACCAAGAGATTCACACCCCGGAGAGATCCAGATGCCCCCTAGCGGT 2705
QY 2986 TTGAAGATTTGAATCCAACTGAGACTCTCACTTTGAAATGGGATCCACGAGCAC 3045
DB 2706 TTCCGAGTCCGCGACCCCAACTGAGACATCACTGGAATGGGATCATCTGAGCAT 2765
QY 3046 CCGAATGCAATTTGAAGAGATCACTTAAAGTATCAGCCAAATTAACAGACACATGAA 3105
DB 2766 CCAAAATGGAATCATATTTGAATCACTCAAAATTTGGGCTTTAAAGGAGC---CAA 2822
QY 3106 TTAGGCCCTCTGTGATTTGAATAATCTGTGCAACAGACGCTGAGCTTTAAATAAT 3165

DB 2823 GTGAGAAAGAGATAGTGGAAAACTTCTCTCCCAATCAGACCAAGTTCAAGGTGCAAGA 2882
3166 TTAATTTTACGACCTGATATAGTTTATTTCTATGACAAACATCAGAGATCAGGA 3225
DB 2883 ACCGACCCCGTGTGACGCTACCGCTTACCTTACGCGCAGGACGAGGAGGCTGTGG 2942
QY 3226 AGTCAATTTACAGAGAGAGATTAAGCACTGTGATGAAGCTGG 3269
DB 2943 GAAGCGGTACAGAGAGATCACCAGACACCCCGAATGAAGGTAG 2986

RESULT 14
AAK51847
ID AAK51847 standard; cDNA; 4694 BP.
XX AAK51847;
AC AAK51847;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 392.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001MO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
XX P-PSDB; AAM78714.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 1; Page 1484-1488; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
XX Sequence 4694 BP; 1161 A; 1340 C; 1292 G; 901 T; 0 U; 0 Other;

Query Match 16.4%; Score 676.6; DB 4; Length 4694;
Best Local Similarity 53.5%; Pred. No. 3.8e-188;
Matches 1690; Conservative 0; Mismatches 1314; Indels 95; Gaps 6;

QY 242 TAGAGCTTCAACCATCACCACCAAGTCTCCAAAAGATTATTAATTTAGCTCGGGAGA 301
DB 7 TCGGCGCGCAACCATCACCACCAAGTCTCCAAAAGATTATTAATTTAGCTCGGGAGA 66
QY 302 AATATTGATTCAGGTGAAGCCAAAGGAAAACCGCCCAAGCTTTTCTGGAACCGTA 361
DB 67 ACATCTGATGAGTGAAGCCAAAGGAAAACCGCCCAAGCTTTTCTGGAACCGTA 126
QY 362 ATGGAGCTATTTGACATGATTAAGACCTCTGTGATCACCATGAAGCTTGACAGGA 421
DB 127 ACAGAGATTTCTTAACATTCGCAAGAGACCCCGGGTGTTCATGAGAGAGGTCTGGGA 186
QY 422 CGCTCATTAATTAATCATCATGAGCGAAGGAAAAGCTGAAGCTTAAGAGATCTATCAGT 481
DB 187 CCTGTGATGATGACTTCCGAGTGGCGGGCGCGCGAGGAATATGAGGGGGAATATCAGT 246
QY 482 GTACAGCAAGAGAGAGAGCGGAGCTGAGTTTCTAATTAATGATGTGCGCCATCA 541
DB 247 GCTTGCGCCGCAACAATTTGACAGGCTGTCTCAATAGATCCGCTGACAGGTCTTA 306
QY 542 GATCAACATTTGTGACCAAGAAAACCTGAACCAATCACACTTCAAAAGTGTCACTT 601
DB 307 AATCTCTGTGTGCGCAAGGAAAACCTGAACCTGTGTGTGTCAAAGAGGCGCTCTT 366
QY 602 TAGTACTTCTGTCAGACCCCAATTTGATTAACCACTTAATTAATTTGATGATGA 661
DB 367 TGACGCTCAGTGAACCCCGCTGAGCTTCCATCCCGGTCAATCTTCTGAGAGACA 426
QY 662 ATTCTTTCAAAAGCTTCCAAAGTGAAGGTTTCAAGTTTGAATGGGACCTT 721
DB 427 GCTTCATGAGCCCATCAACCAAGCAACGTTCTTCAAGGCTTAACGAGCTAT 486
QY 722 ATTTTTCATGCTCTCCAGAGAGACCCGAGAGATATATCTGTTATGCTAGATTYA 781
DB 487 ACTTCTCAAGTATGATGTCAGAGACATGACAGACGATCAAGTTGTAACGCGCTTCC 546
QY 782 ATCAATCTCAACATCAAGAGAGAAACCTATTTCTGTGAAGGTATTTCACTGATG 841
DB 547 ACTTCACCCACACATCCAGAGAAACCTTTTCACTTCAAGGTCTTCAACCCGAG 606
QY 842 AATGAATGACACTTACTGCTAATTTGAGTGAACATGATTTAATGCTTAATCA 901
DB 607 GAGT----- 610
QY 902 GTAGAGAGGCGCACCAATTTTAACTCCAGAGAGATGCAATGAACAAGAGAT 961
DB 611 -TGCAAGAAAGAACCAAGCTTCAATGATCCCGAGGACCGCGAGAGCAAGATGATG 669
QY 962 TAAAGAAATGTGCTTACTGAGTGCATTTGAGAGAGAGCTGCTAACCCCAATTTT 1021
DB 670 TTCTGTGAGATGACCTCTGCTGATGATGATGCTCTCGGGGTCCCAACACAGACATG 729
QY 1022 ACTGGGCAAGAGAAATGGAATGCTAACCCAAAGAGAGAGTATTAAGAACTTGGA 1081
DB 730 CATGTATCAAGAAAGTGGGACCTCCATCTGATGAAGCCCAAGTTGAAGAACTTATTA 789
QY 1082 AAACCTTCAGATCTATGATTTTGAAGAGAGAGCTGGAATTAACCAATGATAGCA 1141
DB 790 AGGCTTCGATATCAAAATGCTCTGAGAAAGATCCGGGAGATTTCTGCGTGGCT 849
QY 1142 AAATGATTAAGAGCAATCAACATACATTTCTGTTAAGTTAAGCGCTCCATCT 1201
DB 850 CCAACAAGATGGGAGAGATTCGCGCACAGATCTCGGTAGAGTAAAGGCTCTCTCTACT 909
QY 1202 GGATACAGCCCTCAAAATCTGTGCTGTCCCGAGAGAGAGAGAGCTTGATCTCA 1261
DB 910 GGCTGAGCAACCAAGAACTTATTTCTGCTCTCGGAGAGATGGAGACTGTGTCTC 969

OY	1262	GAGCTAAATGGCAACCCCAACCCCAAGAAATTAAGTGGTTAAACAAATGAGATGCCAATAGAAA	1321
Db	970	GAGCCAAATGGAAACCCCAAAACCCCACTGTCTCACTGATGATGTGAATGGGAACCTTTGCAAT	1022
OY	1322	TTGCCCTCGATGACCCCGACAGAAAAAATAGATGGCGATACCATTAATTTTTCMAATGTTTC	1381
Db	1030	CGGCACGACCTTAACCCAAACCGTGAGTGGCCGAGACACCATCATCTTCCGGGAGACACC	1089
OY	1382	AAGAAAGATCAAGTGCAGTATATCAGTGCATATGCTCTTAATGAAATATGGAATTTTACTGG	1441
Db	1090	AGATCAGCAGCAGGGCTGTGTATACAGTGCACACCTCCAAAGAGCATGGTACTCGCTGG	1149
OY	1442	CAAAACGCAATTTGTAAATGCTGCTGGTGCCACACAGAAATCTCTCACTGCATCAACACAC	1501
Db	1150	CCAAAGCTTTGTCTAGTGTGTGATGATGGCCGCTCGGATCTGTGGCCCGGAACAGC	1209
OY	1502	TCATACAGAGTCATTTGCAACAGAGCCGTGGCTTTACTAGCTGTGCTCTTTTGGGATCTCTC	1561
Db	1210	TCATTTGAGTGAATCTTTACAAACGGGAGCGCGGTGGAATGCTGCCCTTTCTTTGGGTCTCCA	1265
OY	1562	TCCCAACCATCGAGTGTTTTAAAGAGCTTAAAGAAATGCTCTTTCATGAAATATTTATG	1621
Db	1270	TCCCAACCATCGAGTGTTTTAAAGATGGGCAAGAGCAACCTGGATGTGTGCAACATCAC	1329
OY	1622	TTTTTACATGAATAATGCACTTTTGGAAATCAAAAGATGCTACATGATGCTTTAAAGAAATTC	1681
Db	1330	ATGTTTATGAAACCGCAGTCTGGAAAT-TAAGATGATCCGCAAGAGACACAGGCATTC	1388
OY	1682	CTGTGGCCCAAAAGGACAGTACAGGAATTTATACGTGTGTTCAAAGAAATTAATTAGGGA	1741
Db	1389	TACACCTGTGTGCGCACCAACATCTGTGGCAAAAGCTGAAAACCAAGTCCGCTGGAGGTC	1448
OY	1742	TGGCAAAAGATGAAGTTT-ACCTTACAGCCGGAATATGCAAGTTGTGCAAAAGAGGAGCATG	1800
Db	1449	AAAGACCCCAACAGGATCTTACCGGATGCCCCGAGGACACAGTGGCCAGAAAGGGGACACAG	1508
OY	1801	GTTGTCCTTTGAATGCAAAAGTGAATAATATATCAACCTTATCCCTCACTGTCTGTGGCTG	1860
Db	1509	GTCAGCTGTGAGTGTGGGTGAAGACACACCTCTCCCTGAAATCTCACCGTCTTCTGTGGCTG	1568
OY	1861	AAGGACAAACAGGGAACCTGCCAGTATGAAGGTTCACTGTTTGAACAGATCATCTAGTG	1920
Db	1569	AAGATATGACGAGCCGCTTATATTTGGAACACAGATGAAGAAAGAAAGACATTTGTGACC	1628
OY	1921	GTAAGCTGATGTCAGTGACGATGACAGCGGGAACCTACACGTGTGTGGCCCAACACCATCTG	1980
Db	1629	ATCTTTGGGGTGGGACGAGCGGGGACACAGGGCAGTTACAGTGTGTGCGCCAGCACCGAGTGA	1688
OY	1981	GACAGCGTCTCCGCCACGCGCTGTGCTTACGCTTGTGCTCTTACTTCCATCTCACGCTCC	2040
Db	1689	GACCAAGACCTGGGCCCAAGGCTTACTCTCACCGTGTAGGACGG-----	1730
OY	2041	GTTTACGATGTCCAAATCTCCCTTTTGAATTTAGACATGAACAGATCAACTTGACAAAGT	2100
Db	1731	-----CCAGACCGGCCCCGGGACCTGTGAGCTGACCGACCTGGCCGAGGGAGGC	1778
OY	2101	GTTCAAGCTGTATGGACCCCAAGCGGATGACAAATATAGCCCATTAACAAATTTATCATCTC	2160
Db	1779	GTTGGGCTGACCTGTGATCCCGGGGATGCTTAACAAACGCCCATCAACAGACTAGTGTCTC	1838
OY	2161	GAAATATGAATGCAATGCAACAGCCAGGCGTGTGGACCAACCAACTGAAGTTTCTGGA	2220
Db	1839	CAGTTTGAAGAAAGACAGTTTCCAACTTGGGGTCTGGCAATGACATTCCAATGATACCCGGGC	1898
OY	2221	ACAACGACACAGCCACAGCTGAAGTGTCTCTTAACGGAATCTACTCTTCCGGGTGATG	2280
Db	1899	AGCGTTAATCTAGCGCTCTCTCGGCTGTGCTCCGTAATGCAATACAGTTCGCTGTCAATT	1958
OY	2281	GCAGTGAACAGCATTTGGGAGAGCTTGGCCACAGCGAGCGTCTGACAGTATTTGACGAAA	2340
Db	1959	GCATATCAACGAGGTTGGGAGAGCAACCCACAGCTCCCATCTCGAGCGGTTACGAAACAGT	2018
OY	2341	GCCTCAGAACAGATAAAAACCCCAACAGCTGTGAAAGACTGGGATCAGAGCTGTGATAT	2400

Db	2019	GGAGCACCCCCCGCAGTCCAAATCTGTGTGACGTGAAGGAGAGGGGACCAAGAAAGAACAC	2078
Qy	2401	TTGAGAGATTACGTGGAAAGCCCTTGAATGTGTTTGCATCTTAAATGGACCAGCCTTCACTAC	2460
Db	2079	ATGGAAGATTCAGTGGAGCGCCCATGAATGCCACCTCGGCTTTGGCCCAACTCCGCTAC	2138
Qy	2461	AAAGTTAGCTGGCCCGCAGAAAGATGTGATGATGAATGACATCTGTGTGTGTGGCAAT	2520
Db	2139	ATTGTTCAGATGGAGGCGGAGAGACACTGAGAGGCGCTGGAAACAGTCACAGT---TGG	2195
Qy	2521	GTATTCACAAATATATATGTCTCAGGACGGCAACCTTGTTCATACCTGATCAAGTTACAG	2580
Db	2196	GGCTCTCGCTACGTGTGTGGGACAGACCCCACTTACGTGCTTGTGAGATCCGAGTCCAG	2255
Qy	2581	GCCCTGATGATCATGGGGTTTGCCCGGAGCCAGCTGTAGTCATGGGACATTCGAGAA	2640
Db	2256	GCTGAATATGACTTCGGGAGAGGGCGCTGAGCAGAGTCCGTCATCGGTACTCCGAGAA	2315
Qy	2641	GACCTCCCAATGTGTGCTCTCTGGGAGGTGCGCTGTAATGTGTGAACAGTACTTACG	2700
Db	2316	GATTATCCAGGGCGTGGCCCACTGAAGTTTAAATCCGAGTCATGAACAGACAGCCATC	2375
Qy	2701	GAGGTGACCTGGGACCCAGTACCTCTGAAAAAGCATCCGAGGACACTACAGAGCTATCG	2760
Db	2376	AGCCTCAGTGGAAACCGGCTTACTCCGACAGGTTCAAGGCGCAGCTCAGAGATACCGA	2435
Qy	2761	ATTTCATTGGGAAGACCCAGAGTTCACTTAAAGAAACAGACCTCACATTGGAAAAAG	2820
Db	2436	GCTACTACTGGAGGAGAGACGTTCTGTGAAGAACTGTGGGTGTCTCAGAAAGACAG	2495
Qy	2821	ATCTCTACCTTCCAGGACGACAGACTCATGTGCACTGTTCGCGGGCTTAGACCTTTAC	2880
Db	2496	CAGCCAGCTTCCCTGGTGAACCGCTCGTGGCTGTGTCCGCTCTTCCCTACAGT	2555
Qy	2881	CACATCACACTGAATGTGCCAGTGTGTGAATGGGAAAGGGGAGGGCCAGCCAGCCGTGAC	2940
Db	2556	AACATCAAGCTGGAGATGTGTGTGTCTAATGGGAGAGGTGATGGGCTTCGACGTGAGACC	2615
Qy	2941	AGAGTCTTTAATATCTCCAGAAAGAGTCCCAAGTGTCTCCCTGTCTTTGAAGATTGTGAAT	3000
Db	2616	AAGGATGTCACACCCCGGAAAGAGTACCAAGTCCCTTAGGCGTTTCCAGTCCGCGAG	2675
Qy	3001	CCAACTGTGACTGTCTCATCTTGGAAATGGGATCACCTGAGCCACCCGAAATGCAATTTG	3060
Db	2676	CCCAACTGGAGACAATCAACTGTGAATGGGATCATCTGAGCATCCAAATGGGATCATG	2735
Qy	3061	ACAGAGTACACTTAAAGTATCAGCCAAATTACAGCACATGAAATTAGCCCTCTGTGTA	3120
Db	2736	ATTGTGATACCTCTCAAAATATGTGGCTTTTACGGGAC---CAAAAGTGAAGAACACATA	2792
Qy	3121	GATTGAAATATCTGTGCAACAGACAGCGGTGACCTTTAAAAAATTTAAATTTGACACT	3180
Db	2793	GTGAAAAATCTTCTCTCCCAATCAGACCAAGTTTACGGGTGAAAGAACGAGCCCGTGTCA	2852
Qy	3181	CGATATAAGTTTATTTTCTATGCAAAACATCAGACGATCAGGAAAGTCAATTTACAGAG	3240
Db	2853	CGTACCGCTTTACCTCAAGGCGCAGGACCGAGGTGGGCTCTGGGAAAGCGGTACAGAG	2912
Qy	3241	GAAGCACTAACACTGTGTGATGAAGCTGG	3269
Db	2913	GAGTCACACGACCCCGAATGAAGTGTG	2941

Db 1408 GGGAACTTTGGCAATCGGACCACTTAACCCAAACCGTAGGTGGCCGGAGACACCATCA 1467
QY 1367 TTTTTCATATGTCAGAAAGATCAAGTGCAGTATATCATGTCATATGCTCTAATGAAT 1426
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 1 Wang, B., Williams, H., Du, J. S., Terrett, J. and Kenwright, S.
 Alternative splicing of human NRCAM in neural and nonneural tissues
 JOURNAL Mol. Cell. Neurosci. 10 (5-6), 287-295 (1998)
 MEDLINE 98267566

PubMed 9604207
 REFERENCE 2 (bases 1 to 3900)
 AUTHORS Wang, B.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-1997) Wang B., Department of Medicine, University
 of Cambridge, Addenbrooke's Hospital, POBox 157, Hills Road,
 Cambridge, CB2 2QQ, BRITAIN

FEATURES

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ORIGIN

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ACCESSION AX099489
VERSION AX099489.1 GI:13538577
KEYWORDS
SOURCE Homo sapiens (human)

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Jacobs, K., McCoy, J.M., Lavalie, E.R., Colling-Racie, L.A., Evans, C.,
 Weisberg, D., Treacy, M., Bowman, M.R., Spaulding, V., and Agostino, M.J.
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 1232 TACTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1291
 1081 AAAACCTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 1292 AAAACCTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1351
 1141 AAAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 1352 AAAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
 1201 TGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 1412 TGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471
 1261 AGAGCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 1472 AGAGCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1531
 1321 ATTTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 1532 ATTTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1591
 1381 CAAGAAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
 1592 CAAGAAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1651
 1441 GCAAGAGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 1652 GCAAGAGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1711
 1501 CTCTACAGAGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 1712 CTCTACAGAGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1771
 1561 CTCTACAGAGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 1772 CTCTACAGAGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1831
 1621 GTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
 1832 GTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1861
 1681 CTTGTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 1862 CTTGTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1921
 1741 ATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1770
 1922 ATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1981
 1771 GAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1830
 1982 GAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2041
 1831 CACACCTTATCCCTCACTGTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1890

Db 2042 CACACCTTATCCCTCACTGTCTCTGTGCTGAAGGACAAACAGGGAGCTGCCAGTGATGA 2101
Qy 1891 AGGTTCACGTGTGACGAAGGATCATCTAGTGTAGCTGATGATGACGATGACAGCGGG 1950
Db 2102 AGGTTCACGTGTGACGAAGGATCATCTAGTGTAGCTGATGATGACGATGACAGCGGG 2161
Qy 1951 ACCTACAGCTGTGTGGCCAAACACACTCTGACAGCGGTCTCCGCCAGCGCTGTGTAC 2010
Db 2162 ACCTACAGCTGTGTGGCCAAACACACTCTGACAGCGGTCTCCGCCAGCGCTGTGTAC 2221
Qy 2011 GTTGTGTCTCTACTCACTCACTCCAGCTCCCGTTTACGATGTCCCAATCTCTCTTAC 2070
Db 2222 GTTGTGTCTCTACTCACTCACTCCAGCTCCCGTTTACGATGTCCCAATCTCTCTTAC 2281
Qy 2071 TTGAGACTGACGATCACTTGACAAAGGTTCACTGTCACTGACCCCGAGCGATGAC 2130
Db 2282 TTGAGACTGACGATCACTTGACAAAGGTTCACTGTCACTGACCCCGAGCGATGAC 2341
Qy 2131 AACATAGCCCATTTACAAATTCATCATGATATGATGATGACAGCCAGG 2190
Db 2342 AACATAGCCCATTTACAAATTCATCATGATATGATGATGACAGCCAGG 2401
Qy 2191 CTGTGACACCAACCACTGAAGTTTCTGACACAGACCAAGCCAGCTGAAGCTGTCT 2250
Db 2402 CTGTGACACCAACCACTGAAGTTTCTGACACAGACCAAGCCAGCTGAAGCTGTCT 2461
Qy 2251 CCTTACGTAACTACTCTTCGCGGTGATGGAGTGAAGAGATTTGGAAAGCTTGCC 2310
Db 2462 CCTTACGTAACTACTCTTCGCGGTGATGGAGTGAAGAGATTTGGAAAGCTTGCC 2521
Qy 2311 AGCGAGGCGCTGAGAGATTTTGAAGAACCTCGAACCAAGTAAACCCACAGCT 2370
Db 2522 AGCGAGGCGCTGAGAGATTTTGAAGAACCTCGAACCAAGTAAACCCACAGCT 2581
Qy 2371 GTGGAAGACTGGGATCAGAGCTGATTAATTGGAGATTAAGTGAAGCTTTGAATGT 2430
Db 2582 GTGGAAGACTGGGATCAGAGCTGATTAATTGGAGATTAAGTGAAGCTTTGAATGT 2641
Qy 2431 TTGCAATCTAATGGGCGAGGCTTGATCAAAAGTTAGCTGGGCGCAGAAAGTGTGAT 2490
Db 2642 TTGCAATCTAATGGGCGAGGCTTGATCAAAAGTTAGCTGGGCGCAGAAAGTGTGAT 2701
Qy 2491 GATGATGACATCTGTGTGTGGCAAAATGTATCCAAATATATGTCTCAGGACAGCA 2550
Db 2702 GATGATGACATCTGTGTGTGGCAAAATGTATCCAAATATATGTCTCAGGACAGCA 2761
Qy 2551 ACCTTGTTCATCTGATCAAAAGTTCAAGCCCTGAATGACATGGGGTTTCCCCGAG 2610
Db 2762 ACCTTGTTCATCTGATCAAAAGTTCAAGCCCTGAATGACATGGGGTTTCCCCGAG 2821
Qy 2611 CCAGCTGTGTCACTGGGACATTTCTGAGAGAGACCTCCCAATGGTGTCTCTGGGAAGCTG 2670
Db 2822 CCAGCTGTGTCACTGGGACATTTCTGAGAGAGACCTCCCAATGGTGTCTCTGGGAAGCTG 2881
Qy 2671 CGTGTGAATGTGTGAACAGTACTTACCGGAGTCACTGGGACCCAGTACTCTGAA 2730
Db 2882 CGTGTGAATGTGTGAACAGTACTTACCGGAGTCACTGGGACCCAGTACTCTGAA 2941
Qy 2731 AGCATCCGAGACCTCAAGGCTATCGGATTTACTATTGGAAGACCCAGAGTTACTCT 2790
Db 2942 AGCATCCGAGACCTCAAGGCTATCGGATTTACTATTGGAAGACCCAGAGTTACTCT 3001
Qy 2791 AAAAGAAACAGAGCTGACATTTGAGAAAAGATCTCACTCCCAAGGACAGACTCAT 2850
Db 3002 AAAAGAAACAGAGCTGACATTTGAGAAAAGATCTCACTCCCAAGGACAGACTCAT 3061
Qy 2851 GGCATGTTCGGGGCTAGAGCCTTTAGCACTACACACTGATGTCCGAGTGTCAAT 2910
Db 3062 GGCATGTTCGGGGCTAGAGCCTTTAGCACTACACACTGATGTCCGAGTGTCAAT 3121
Qy 2911 GGGAAAGGGAGGGCCAGCAGCCTTGAAGAGTCTTTATATCTCAGAGAGAGTCCC 2970
Db 3122 GGGAAAGGGAGGGCCAGCAGCCTTGAAGAGTCTTTATATCTCAGAGAGAGTCCC 3181

Qy 2971 AGTGTCCCTCGTCTTTGAAGTTGTGATCCAACTGAGACTCTCTCATTTGGAAATG 3030
Db 3182 AGTGTCCCTCGTCTTTGAAGTTGTGATCCAACTGAGACTCTCTCATTTGGAAATG 3241
Qy 3031 GATCCAGGACCCGAAATGGCAATTTTGAAGAGTACACTTAAAGTATGACCAAT 3090
Db 3242 GATCCAGGACCCGAAATGGCAATTTTGAAGAGTACACTTAAAGTATGACCAAT 3301
Qy 3091 AACAGACACATGATTTAGGCGCTCTGGATTTGAATTTCCGCCAACAGACAGG 3150
Db 3302 AACAGACACATGATTTAGGCGCTCTGGATTTGAATTTCCGCCAACAGACAGG 3361
Qy 3151 TGACCTTTAAAAATTTAAATTTTCACTGATTAAGTTTATTTATGACAAACA 3210
Db 3362 TGACCTTTAAAAATTTAAATTTTCACTGATTAAGTTTATTTATGACAAACA 3421
Qy 3211 TCAGCAGATCAGGAAGTCAATTTACAGAGAGCAGTAACTGTGTGATGAGCTGT 3270
Db 3422 TCAGCAGATCAGGAAGTCAATTTACAGAGAGCAGTAACTGTGTGATGAGCTGT 3481
Qy 3271 ATTCTTCACCTGATGTAGTGGCAGCAAGTTCAAGCTGTAATACAGGATCAGCAAT 3330
Db 3482 ATTCTTCACCTGATGTAGTGGCAGCAAGTTCAAGCTGTAATACAGGATCAGCAAT 3510
Qy 3331 CTTACTGTGAGCTGTGAGACTATGCAATATCACTGGGAATATGAGGACAGAG 3390
Db 3511 CTTACTGTGAGCTGTGAGACTATGCAATATCACTGGGAATATGAGGACAGAG 3510
Qy 3391 CATGTGAACCTTTATGTTGAATATGCTGTAGCAGCAGCAAGAAATGAGAAAGAA 3450
Db 3511 CATGTGAACCTTTATGTTGAATATGCTGTAGCAGCAGCAAGAAATGAGAAAGAA 3510
Qy 3451 ATTGAATATGTTCTCGAGAGCTTTTGGGTTAAAGGCTTAATGACAGAAACAGCATAC 3510
Db 3511 ATTGAATATGTTCTCGAGAGCTTTTGGGTTAAAGGCTTAATGACAGAAACAGCATAC 3510
Qy 3511 AAAGTTGAGTTGTGCTGTGGGGAGCTGTGTTTGTGAGTTGAGAGATGTGTTGAG 3570
Db 3511 AAAGTTGAGTTGTGCTGTGGGGAGCTGTGTTTGTGAGTTGAGAGATGTGTTGAG 3510
Qy 3571 ACAGGCCAGGATGGCAAGCCGCGAGGTGATTTGCAACTCAGGCGTGGTTCAATGGT 3630
Db 3511 ACAGGCCAGGATGGCAAGCCGCGAGGTGATTTGCAACTCAGGCGTGGTTCAATGGT 3562
Qy 3631 CTGATGTGTGCTGTCTCTCTTATCTTAATTTTGTGATTTGTTGTCTTACAGAGA 3690
Db 3562 CTGATGTGTGCTGTCTCTCTTATCTTAATTTTGTGATTTGTTGTCTTACAGAGA 3622
Qy 3691 AACAGGGTGTAAATATCAGTTAAAGAAAGAGATGCCATGCTGACCTGAAATC 3750
Db 3622 AACAGGGTGTAAATATCAGTTAAAGAAAGAGATGCCATGCTGACCTGAAATC 3682
Qy 3751 CAGCTTATGAGAGAGATGATGGGCACTTTGGAATACAGTATGACAGAGACCAAG 3810
Db 3682 CAGCTTATGAGAGAGATGATGGGCACTTTGGAATACAGTATGACAGAGACCAAG 3742
Qy 3811 CCTTGAAGAAAGAGTGAATCTCTCAGACAGAGCTGTGAAGAAAGAGATAGTAC 3870
Db 3742 CCTTGAAGAAAGAGTGAATCTCTCAGACAGAGCTGTGAAGAAAGAGATAGTAC 3802
Qy 3871 GACAGCTTATGATGATGAGAGAGGGGTAAATGCGCAGTTCAATGAGAGATGCTCTT 3930
Db 3802 GACAGCTTATGATGATGAGAGAGGGGTAAATGCGCAGTTCAATGAGAGATGCTCTT 3862
Qy 3931 ATTGAACATACAGTGTGTAAGAAAGAAAGCGGCTGAAGAAAGCAAGTCTCAGAG 3990
Db 3862 ATTGAACATACAGTGTGTAAGAAAGAAAGCGGCTGAAGAAAGCAAGTCTCAGAG 3922
Qy 3991 GCACTTCTCTCTGTAAGAGCAGTGAATCTTTGTTTAAATTTTAAAGCTCTTGGCAATA 4050
Db 3922 GCACTTCTCTCTGTAAGAGCAGTGAATCTTTGTTTAAATTTTAAAGCTCTTGGCAATA 3982

QY	1501	CTCTACCAAGGTCATTGGCAAAACAAGGCTGCTTTACAGACCTGAGCTTCTTTGGGCTCCCT	1500
Db	1712	CTCTACCAAGGTCATTGGCAAAACAAGGCTGCTTTACAGACCTGAGCTTCTTTGGGCTCCCT	1711
QY	1561	CTCCCAACCATCGAGTGGTTTAAAGAGCTAAAGAGAGTGCCTTTCATGAAGATATTTAT	1620
Db	1772	CTCCCAACCATCGAGTGGTTTAAAGAGCTAAAGAGAGTGCCTTTCATGAAGATATTTAT	1831
QY	1621	GTTTTCACATGAAATATGAACTTTGGAAATCAAAGATGCTACATGATGTTTAAAGAAATT	1680
Db	1832	GTTTTCACATGAAATATGAACTTTGGAAATCAAAGATGCTACATGATGTTTAAAGAAATT	1861
QY	1681	CCTGTGGCCCAAAAGAGACATGACAGAACTTATACGTGTGTGCAGAGATATAATTAGGG	1740
Db	1882	CCTGTGGCCCAAAAGAGACATGACAGAACTTATACGTGTGTGCAGAGATATAATTAGGG	1921
QY	1741	ATGSCAAGAATGAAGTTCCTT-----ACAAGCC	1770
Db	1922	ATGSCAAGAATGAAGTTCCTT-----ACAAGCC	1981
QY	1771	GAAATGACAGTGTGCAAAAGAGGAGACATGGTGTCTTGAATGCAAGTGAACATGAT	1830
Db	1982	GAAATGACAGTGTGCAAAAGAGGAGACATGGTGTCTTGAATGCAAGTGAACATGAT	2041
QY	1831	CACACCTTATCCCTCACTGCTCTGTGGCTGAAGCAACAAGGAACTGCCAGTATGAA	1890
Db	2042	CACACCTTATCCCTCACTGCTCTGTGGCTGAAGCAACAAGGAACTGCCAGTATGAA	2101
QY	1891	AGGTTCACCTGTTGACAAAGATCATCTAGTGGTACGTATGTCACTGACATGACAGCGGG	1950
Db	2102	AGGTTCACCTGTTGACAAAGATCATCTAGTGGTACGTATGTCACTGACATGACAGCGGG	2161
QY	1951	ACCTACACGTGTGTGGCCCAACAACAACACTGTGACAGCGTCTCGCCAGCGCTGTCTTAGC	2010
Db	2162	ACCTACACGTGTGTGGCCCAACAACAACACTGTGACAGCGTCTCGCCAGCGCTGTCTTAGC	2221
QY	2011	GTTGTGCTCCTTACCTCACACTCAGCTCCCGTTTACGATGTGCCAAATCCTTCCTTTGAC	2070
Db	2222	GTTGTGCTCCTTACCTCACACTCAGCTCCCGTTTACGATGTGCCAAATCCTTCCTTTGAC	2281
QY	2071	TTAGAACTGACAGATCAACTTGACAAAAGTGTTCAGCTGATGAGACCCAGGCGGATGAC	2130
Db	2282	TTAGAACTGACAGATCAACTTGACAAAAGTGTTCAGCTGATGAGACCCAGGCGGATGAC	2341
QY	2131	AACAAATAGCCCCCATTAACAAATTCATTCATCGAATAAGAAATGCAACAACAGG	2190
Db	2342	AACAAATAGCCCCCATTAACAAATTCATTCATCGAATAAGAAATGCAACAACAGG	2401
QY	2191	CTGTGGCACCAACCAACTGAAATTTCTGGAAACAAGACAAGCCAGCTGAAGCTGTCT	2250
Db	2402	CTGTGGCACCAACCAACTGAAATTTCTGGAAACAAGACAAGCCAGCTGAAGCTGTCT	2461
QY	2251	CCTTACGGAACCTACCTCTCCGCTGTGATGCGAGTGAACAACATTTGGGAAAGCTTGCC	2310
Db	2462	CCTTACGGAACCTACCTCTCCGCTGTGATGCGAGTGAACAACATTTGGGAAAGCTTGCC	2521
QY	2311	AGCGAGCGCTGAGCAGATATTGACGAAGAGCTTCAACAACGATATAAACCCCAACGCT	2370
Db	2522	AGCGAGCGCTGAGCAGATATTGACGAAGAGCTTCAACAACGATATAAACCCCAACGCT	2581
QY	2371	GTGGAAGACCTGGGATCAGAGCTGATATAATTGGAGATTACGTGGAAACCTTGAATGGT	2430
Db	2582	GTGGAAGACCTGGGATCAGAGCTGATATAATTGGAGATTACGTGGAAACCTTGAATGGT	2641
QY	2431	TTGCAATCTAATGGGCCAGGCGCTTGACGAAAGTTAGCTGGCGCAGAAAGATGCTGAT	2490
Db	2642	TTGCAATCTAATGGGCCAGGCGCTTGACGAAAGTTAGCTGGCGCAGAAAGATGCTGAT	2701
QY	2491	GATGAATGACATCTGTGTGTGTGGCAATGTATCCAAATATATGTCTCAGGCAACGCA	2550
Db	2702	GATGAATGACATCTGTGTGTGTGGCAATGTATCCAAATATATGTCTCAGGCAACGCA	2761

OY	2551	ACCTTTTGTCATCACTCGATCCAAAGTTCAGGCCCTGAAATGACAATGGGGTTTTGC	CCCCAG	261
Dd	2762	ACCTTTGTTCATACTGATCCAAGTTCAGGCCCTGTAATGACATGGGGTTTTGC	CCCCAG	2821
OY	2611	CCACTGTAGTCATGGGACATTCTGAGAGAAGCCTCCCAAATGGTGCTCCTGGGAACGTG	2670	
Dd	2882	CCACTGTAGTCATGGGACATTCTGAGAGAAGCCTCCCAAATGGTGCTCCTGGGAACGTG	2881	
OY	2671	CGTGTGAATGTGTGAACAGTACCCTTAGCCGAGGTGCACTGGGACCCAGTACCTCTGAAA	2730	
Dd	2882	CGTGTGAATGTGTGAACAGTACCCTTAGCCGAGGTGCACTGGGACCCAGTACCTCTGAAA	2941	
OY	2731	AGCATCCGAGAGACACTACAAAGGCTATCCGATTTTACTAATTTGAAAGAACCCGAGTCACT	2790	
Dd	2942	AGCATCCGAGAGACACTACAAAGGCTATCCGATTTTACTAATTTGAAAGAACCCGAGTCACT	3001	
OY	2791	AAAAGAAACAGACSTCACATTGAGAAAAAAGATCCTCACTTCCTCCAGGACACAAAGCTCAT	2850	
Dd	3002	AAAAGAAACAGACSTCACATTGAGAAAAAAGATCCTCACTTCCTCCAGGACACAAAGCTCAT	3061	
OY	2851	GGCATGTTGCCGGGGCTAGAGCCCTTTAGCCACTACACACTGAAATGTCCGATGCTCAT	2910	
Dd	3062	GGCATGTTGCCGGGGCTAGAGCCCTTTAGCCACTACACACTGAAATGTCCGATGCTCAT	3121	
OY	2911	GGGAAAGGGAGGGGCCCAAGCCACGCCCTGACAGAGCTTTTAATTAATCCAGAAAGATGCC	2970	
Dd	3122	GGGAAAGGGAGGGGCCCAAGCCACGCCCTGACAGAGCTTTTAATTAATCCAGAAAGATGCC	3181	
OY	2971	AGTGTCTCCCTGCTGTTTGAAGATTTGTGATTCCAACA CTGACCTCTCACTTTTGGAAATGG	3030	
Dd	3182	AGTGTCTCCCTGCTGTTTGAAGATTTGTGATTCCAACA CTGACCTCTCACTTTTGGAAATGG	3241	
OY	3031	GATCCACCGAGCCACCCGAATGGCATTTTGA CAGAGTACCTTTAAAGTATCAGCCAA TT	3090	
Dd	3242	GATCCACCGAGCCACCCGAATGGCATTTTGA CAGAGTACCTTTAAAGTATCAGCCAA TT	3301	
OY	3091	AACAGCACATGAAATTAAGGCCCTCTGTGTAGATTGTA AATTCCTGCGCAACAGACACGG	3150	
Dd	3302	AACAGCACATGAAATTAAGGCCCTCTGTGTAGATTGTA AATTCCTGCGCAACAGACACGG	3361	
OY	3151	TGCACTTTAAAAAATTTAAATTTTACAGACCTCGATATATAGTTTATTTCTATGACACAACA	3210	
Dd	3362	TGCACTTTAAAAAATTTAAATTTTACAGACCTCGATATATAGTTTATTTCTATGACACAACA	3421	
OY	3211	TCAGCAGGATCAGGAGTCAAAATTACAGAGAGACAGTACAACTGTGATGAAAGCTGCT	3270	
Dd	3422	TCAGCAGGATCAGGAGTCAAAATTACAGAGAGACAGTACAACTGTGATGAAAGCTGCT	3481	
OY	3271	ATTCTTCCACTGTAATGTAGTGTCAGGCAAAAGTTCAAGCTGTAAATACAGAGATCAGCAAT	3330	
Dd	3482	ATTCTTCCACTGTAATGTAGTGTCAGGCAAAAGTTCAAGCTGTGTAAATACAGAGATCAGCAAT	3510	
OY	3331	CTTACTGTGAGTGTGCTGAGACCTATAGCCAATATCA GTTTGGAAATATGAGGGACCAAG	3390	
Dd	3511	-----	3510	
OY	3391	CATGTGAAC TTTATGTGTGAATATGTGTAGCAGGACAGCAAAAGAAATGAGAAAAA GAA	3450	
Dd	3511	-----	3510	
OY	3451	ATTGTAAATGTTCTCGAGACTCTTTGGGTTAAAGGGCTCTAATGCCAGAACAGCATAC	3510	
Dd	3511	-----	3510	
OY	3511	AAAGTTGAGTTGGTGTCTGTGGGGACTCGTTTGTGTAGTTCAAGAGATGTGTGGAG	3570	
Dd	3511	-----	3510	
OY	3571	ACAGAGCCAGAGATGCAAGCCGGCAGGTGATTTGCAACTCAGGGCTGGTTCAATTTGCT	3630	
Dd	3511	-----AGGATGCGAAAGCCGGCAGGTGATTTGCAACTCAGGGCTGGTTCAATTTGCT	3562	
OY	3631	CTGATGTGTGCTGTGTCTCTCTTATCTTAATTTTGTGTGATGTGTGCTTCTCATCAGAGA	3690	

Db 780 TGTACGACGAGGACGAGCGAGCTGCAGTTCCTAATATACATTTGTTCGCCCATCC 839
QY 541 AGATCCCACTTGTGACCAAGAAAACTTGAAACAATGCACTTCAAAAGTGTGACGT 600
Db 840 AGATCCCACTTGTGACCAAGAAAACTTGAAACAATGCACTTCAAAAGTGTGACGT 899
QY 601 TTAGTACTTCCCTGACAGACCCCAATGGAATTAACAACAATTAATTTTGGATGAT 660
Db 900 TTAGTACTTCCCTGACAGACCCCAATGGAATTAACAACAATTAATTTTGGATGAT 959
QY 661 AATTCCTTTCAAAAGACTTCCACAAGAGTGAAGATTCTCAAGSTTTGAATGGGACCTT 720
Db 960 AATTCCTTTCAAAAGACTTCCACAAGAGTGAAGATTCTCAAGSTTTGAATGGGACCTT 1019
QY 721 TATTTTCCAAATGCTCCGACAGAGCAACCCGGAAGACTATATCTGTATGCTAGATT 780
Db 1020 TATTTTCCAAATGCTCCGACAGAGCAACCCGGAAGACTATATCTGTATGCTAGATT 1079
QY 781 AATCATACTCAACCAATACAGACAGAAACAATTTCTGTGAAGGTGATTTCACTGAT 840
Db 1080 AATCATACTCAACCAATACAGACAGAAACAATTTCTGTGAAGGTGATTTCACTGAT 1139
QY 841 GAATTAATGACACTATAGCTGCTAATTTGATGACACTGAGTTTATGCTGCTAATCA 900
Db 1140 GAATTAATGACACTATAGCTGCTAATTTGATGACACTGAGTTTATGCTGCTAATCA 1199
QY 901 AGTAGAGAGAGGCAACAATTTTAACTCCAGAAAGGCAATGCAAGTAACAAGAGAA 960
Db 1200 AGTAGAGAGGCAACAATTTTAACTCCAGAAAGGCAATGCAAGTAACAAGAGAA 1259
QY 961 TTAAGAGAAATGTGCTTTCATCTGAGAGTGCATTCAGAAAGACTGCTCAATTTAT 1020
Db 1260 TTAAGAGAAATGTGCTTTCATCTGAGAGTGCATTCAGAAAGACTGCTCAATTTAT 1319
QY 1021 TACTGGGCAAGAGAAATGGAATGCTACCAAAAAACAAGACTTTATTAAGAACTTTGAG 1080
Db 1320 TACTGGGCAAGAGAAATGGAATGCTACCAAAAAACAAGACTTTATTAAGAACTTTGAG 1379
QY 1081 AAAACCTTGACATCTTCACTGTTTCAAGAGAGACTGGAATTAACAATGATATGGA 1140
Db 1380 AAAACCTTGACATCTTCACTGTTTCAAGAGAGACTGGAATTAACAATGATATGGA 1439
QY 1141 AAAATGACTTAGAGACCATCAACATCAATTTCTGTTAAGATTAAAGCGGCTCCATAC 1200
Db 1440 AAAATGACTTAGAGACCATCAACATCAATTTCTGTTAAGATTAAAGCGGCTCCATAC 1499
QY 1201 TGGATCAAGCCCTCTAAATCTTGTGCTGTCCCGAGAGAGATGGGACTTGTATCTGC 1260
Db 1500 TGGATCAAGCCCTCTAAATCTTGTGCTGTCCCGAGAGAGATGGGACTTGTATCTGC 1559
QY 1261 AGAGCTAATGGCAACCCCAAACTTGAATGCTGTTAACAATGGAATGCCAATGAA 1320
Db 1560 AGAGCTAATGGCAACCCCAAACTTGAATGCTGTTAACAATGGAATGCCAATGAA 1619
QY 1321 ATTGCCCTGATGACCCCAAGCAAAAAATAGATGCGATACATTAATTTTCAAAATGTT 1380
Db 1620 ATTGCCCTGATGACCCCAAGCAAAAAATAGATGCGATACATTAATTTTCAAAATGTT 1679
QY 1381 CAAGAAAGATCAAGTGAATATCACTGATGATGCTCTTAATGAATATGATATTTACG 1440
Db 1680 CAAGAAAGATCAAGTGAATATCACTGATGATGCTCTTAATGAATATGATATTTACG 1739
QY 1441 GCAAGGCAATTTGTAATGTGCTGAGGCAACAATGCTGCACTGCACTGCAACACA 1500
Db 1740 GCAAGGCAATTTGTAATGTGCTGAGGCAACAATGCTGCACTGCACTGCAACACA 1799
QY 1501 CTCCTACAGGTCTATTCACCAAGCGCTGCTTTTCTAGACTGTGCTCTTCTTGGGTCTCT 1560
Db 1800 CTCCTACAGGTCTATTCACCAAGCGCTGCTTTTCTAGACTGTGCTCTTCTTGGGTCTCT 1859
QY 1561 CTCCTACCAATCGATGCTTTTAAAGAGCTAAAGAGAGTCTCTTATGAATATTTAT 1620
Db 1860 CTCCTACCAATCGATGCTTTTAAAGAGCTAAAGAGAGTCTCTTATGAATATTTAT 1919

QY 1621 GTTTACATGAAATATGAACTTTGGAAATCAAAAGATCTACATGATGCTTTAAAGAAAT 1680
Db 1920 GTTTACATGAAATATGAACTTTG-----GAAAT 1949
QY 1681 CCTGTGGCCCAAGAGACATGACAGAACTTATACGTGTGTCAGAGAAATTAATAGG 1740
Db 1950 CCTGTGGCCCAAGAGACATGACAGAACTTATACGTGTGTCAGAGAAATTAATAGG 2009
QY 1741 ATGGCAAGAAATGAAGTCACTT-----ACAGCC 1770
Db 2010 ATGGCAAGAAATGAAGTCACTTACAAATCAAAGATCTACATGATGCTTTAAACAGCC 2069
QY 1771 GAATATGCAAGTGTGTCAGAAAGGAGCATGTGTCTTTGAATGCAAGTGAACATGAT 1830
Db 2070 GAATATGCAAGTGTGTCAGAAAGGAGCATGTGTCTTTGAATGCAAGTGAACATGAT 2129
QY 1831 CACACCTTATCCCTCACTGTCTGTGCTGTAAGGCAACAGGAACTGCCCATGATGA 1890
Db 2130 CACACCTTATCCCTCACTGTCTGTGCTGTAAGGCAACAGGAACTGCCCATGATGA 2189
QY 1891 AGGTCACTGTGTAAGAGATCATAGTGTGAGCTGATGTCAAGTACGATGACAGCGG 1950
Db 2190 AGGTCACTGTGTAAGAGATCATAGTGTGAGCTGATGTCAAGTACGATGACAGCGG 2249
QY 1951 ACCTACAGGTGTGTCAGCAACAACACTGGAACAGCGCTCCGCAAGCGCTGTGCTTAC 2010
Db 2250 ACCTACAGGTGTGTCAGCAACAACACTGGAACAGCGCTCCGCAAGCGCTGTGCTTAC 2309
QY 2011 GTTGTGCTCTCACTCAACCTCCAGCTCCGTTTACGATGTCCAAATCTCTCTTAC 2070
Db 2310 GTTGTGCTCTCACTCAACCTCCAGCTCCGTTTACGATGTCCAAATCTCTCTTAC 2339
QY 2071 TTAGAATGACAGATCACTTGACAAAGTGTACGTGATGAGACCCGAGGAGTAC 2130
Db 2340 TTAGAATGACAGATCACTTGACAAAGTGTACGTGATGAGACCCGAGGAGTAC 2399
QY 2131 AACATATGCCCCCATTAACAAATTCATCATGATATGAAATGCAATGCAAGCCAGG 2190
Db 2400 AACATATGCCCCCATTAACAAATTCATCATGATATGAAATGCAATGCAAGCCAGG 2459
QY 2191 CTGTGGCAACCAAACTGAAAGTTCTGGAACAAGACCAAGCCCACTGATGCT 2250
Db 2460 CTGTGGCAACCAAACTGAAAGTTCTGGAACAAGACCAAGCCCACTGATGCT 2519
QY 2251 CCTTACGTAATCTCTTCCGCGTGAATGGAGGAAACAGATTTGGAGAGCTTGGCC 2310
Db 2520 CCTTACGTAATCTCTTCCGCGTGAATGGAGGAAACAGATTTGGAGAGCTTGGCC 2579
QY 2311 AGCGAGGCGTGTGACAGATTTTGAAGAAAGCTTCAAGACAGATTAATAACCCCAAGCT 2370
Db 2580 AGCGAGGCGTGTGACAGATTTTGAAGAAAGCTTCAAGACAGATTAATAACCCCAAGCT 2639
QY 2371 GTGGAAGACGTGGATCAAGGCTGTATATTTGAGATTAAGTGAAGCCCTTGAATGCT 2430
Db 2640 GTGGAAGACGTGGATCAAGGCTGTATATTTGAGATTAAGTGAAGCCCTTGAATGCT 2699
QY 2431 TTGGAATCTAATGGGCGAGGCTTCAAGTAAAGTTACTGGCGCAGAAAGATGAT 2490
Db 2700 TTGGAATCTAATGGGCGAGGCTTCAAGTAAAGTTACTGGCGCAGAAAGATGAT 2759
QY 2491 GATGAATGACATCTGTGTTGTGCAATATGATCAAAATATATTTCTCAGGACAGCA 2550
Db 2760 GATGAATGACATCTGTGTTGTGCAATATGATCAAAATATATTTCTCAGGACAGCA 2819
QY 2551 ACCTTGTTCATACCTGATCAAGCTTCAAGGCTGAAATGACATGGGTTTGGCCGAG 2610
Db 2820 ACCTTGTTCATACCTGATCAAGCTTCAAGGCTGAAATGACATGGGTTTGGCCGAG 2879
QY 2611 CCAAGTGTATGATGAGACATTTCTGAGAGAAACCTCCAAATGAGCTCTGAGGAGG 2670
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 ACCESSION AB002341 GI:2224626
 VERSION KIAA0343.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS Nagase, T., Ishikawa, K., Nakajima, D., Ohira, M., Seki, N., Miyajima, N., Tanaka, A., Kocani, H., Nomura, N. and Ohara, O.
 TITLE Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
 JOURNAL DNA Res. 4 (2), 141-150 (1997)
 MEDLINE 97349984
 PUBMED 9205841
 REFERENCES
 AUTHORS Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.
 TITLE Direct Submision
 JOURNAL Submitted (28-MAR-1997) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yama, Kisarazu, Chiba 292-0812, Japan
 (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
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ORIGIN

Query Match 78.2%; Score 3233.6; DB 9; Length 6218;

Best Local Similarity 89.4%; Pred. No. 0;

Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;

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QY 361 AATGAGACTCATTTTGAATCATGATTAAGACCTCTGTGTCAACATGAAGCCTGGCAGAGA 420
DB 661 AATGAGACTCATTTTGAATCATGATTAAGACCTCTGTGTCAACATGAAGCCTGGCAGAGA 720
QY 421 AGCCTCATATTAACATCATGAGCGAAAGGAAAGCTGAACCTTATGAAGAAGTCTATCG 480
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Db	2074	CACACCTTATCCCTCACTGTCTGTGTGCTGAAGACAACAGGAACTGCCAGTGATGAA	2133
Oy	1891	AGGTTCACTGTGTAACAAGATCATTACTGGTAGTGATGTCACAGGAGATGACAGCGGG	1956
Db	2134	AGGTTCACTGTGTAACAAGATCATTACTGGTAGTGATGTCACAGGAGATGACAGCGGG	2193
Oy	1951	ACCTTACAGGTGTGTGGCCAACAACAACCTGTGACAGCGCTCCGACAGCGCTGTGCTTACG	2010
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Db	2854	CCAGCTGTAGTCATGGGACATTTCTGGAGAAGACCTCCCAATGTGGCTCTTGGAACGTG	2913
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Db	341	CTTCAAGATCCCTGCGATGAAAAATTATTTAAAGCCGCACAC-----CATCT	389						
QY	60	TTTGTGAAGAGAAAGAAATTCAGTGTGTGAGTCTCAGCAGAGTTAAGCTAATGCA	119						
Db	390	TCCGTGAGAGAAAGAAATTCCTGCGTGGGTCTCAGCAGAGTGAAGCTGATGCA	449						
QY	120	GCTTAAATTAATGCGGAAAAAGAGCGCTTATCTGCGGGGAGAGTGGCCCTGATCTCTT	179						
Db	450	GCTTAAATTAATGCGGAAAAAGAGCACTTATCTGAGGGAGAGTGGCCCTGATCTCTT	509						
QY	180	CCTGTCAGATGATTAATGTGATCGAAGTACCTCTTGATTCACAAAATTCTTGAAAGCTT	239						
Db	510	CTGTGCGAGATGATCAGCGCGCTGAGTGTCTCTGATC-----T	551						
QY	240	GGTACAGCTTCACACATCAACCCAAAGTCTCCAAAAGATTACATTAATGACCTCGGGA	299						
Db	552	GGTACACCTTCACACATCACTCAACAGTCAACAAAAGATCACTCATTTGACCTCGGGA	611						
QY	300	GAAATTTGTATCCAGTGTGAAGCCAAAGGAAACCGCCCCCAAGCTTTTCTGAGACCG	359						
Db	612	GAAATTTGTATCCAGTGTGAAGCCAAAGGAAACCTCCCAAGCTTTTCTGAGACTCG	671						
QY	360	TAATGGGACTATTTTGAATCGATTAAGAACCTCTGTGATCAGTAAAGCTGGCAGAG	419						
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Db	792	GTTGACGTCAGAAAGCAAGCGTGAAGCTGCTGCTCCAAATPACTTGTGTCCGCCATC	851						
QY	540	CAGATTCACATTTGAGACCAAGAAACCTTGAACCAATCACACTTGAAGTGTGACGTC	599						
Db	852	TAGGTACCTCTTGTGAGACCAAGAAAGCTTGAACCTATGATCTCCAGATGGGACGTC	911						
QY	600	TTTGAATCTTCCCTGACAGACCCCAATTTGATTAACACACTTAATATTTTGGATGGA	659						
Db	912	ATTGATCTTCCATGTTAGGCTCCGATTTGATTAACCTCCGCCCAATTAATTTTGGATGGA	971						
QY	660	TAAATCTCTTGAAGACTTCCACAAAGTGAAGATTTCTCAGGTTTGAATGGGACCT	719						
Db	972	TAAATCTCTTGAAGACTTCCACAGAGTGAAGCGGTTTCCCAAGGCTTAATGAGACCT	1031						
QY	720	TTAATTTTCCAAATCTCCCAAGAGGACACCCCGGAAGACATATCTGTTATGCTAGATT	779						
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QY	840	TGAATGATGACATATAGCTGTAATTTGATGTAACATGAGATTTTATGCTGTAATATC	899						
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QY	900	AAGTATGAGAGGCGCACCAATTTTATATCTCCAGAAAGCAATTCAGATTAACAAAGAGA	959						
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QY	960	ATTAAAGGAATGCTTTCACTGAGATGATTCGAGAAAGACGTGCTACCCCAATTAAT	1019						
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Db	2262	AACCTTACGTTGTGTGCGCAACCACTGAGACAGTCTCTCCGCAAGCGCTGTGTAG	2321
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DEFINITION Rattus norvegicus ankyrin binding cell adhesion molecule NrCAM
(NrCAM) mRNA, alternatively spliced form, partial cds.
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ACCESSION U81037
VERSION U81037.1 GI:1842430
KEYWORDS
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4044)
AUTHORS Davis,J.O., Lambert,S. and Bennett,V.
TITLE Molecular composition of the node of Ranvier: identification of
ankyrin-binding cell adhesion molecules neurofascin (mucin+/chird
FnIII domain-) and NrCAM at nodal axon segments
JOURNAL J. Cell Biol. 135 (5), 1355-1367 (1996)
MEDLINE 97103184
PubMed 8947556
REFERENCE 2 (bases 1 to 4044)
AUTHORS Davis,J.O., Lambert,S. and Bennett,V.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1996) Howard Hughes Medical Institute, Duke
University, PO Box 3892, Durham 27710, USA
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ORIGIN

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 Db 2077 GGGCTGTGCAACCAACCACTGAAGTTTCTGGAACACAGACCAAGCCAGCTGAAGCTG 2136
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 Db 2137 TCTCTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2196
 Oy 2308 CCAAGAGAGAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2367
 Db 2197 CCAAGAGAGAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2256
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 Db 2257 GCTGTGGAAGAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2316

OY	2428	GGTTTCGAACTTAAATGGGCGCAGGCGCTTACGACAAAGATTAGCTGGCGCCAGAAAGATAGT	2487
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OY	2488	GATGATGAATGAGACATCTGTGGTTGTGGCAATGTATCCAAATATATTTGTCTCAGGACG	2547
Db	2377	GACGATGAATGAGAGTCTGTGGTTGTGGCCAAATGTATCCAAATATATTTGTCTTGCGACA	2436
OY	2548	CCAACTTTGTTCCATACCTGTATCAAAGTTCAAGGCCCTGAATGCAATGGGGTTTGCCCC	2607
Db	2437	CCAACTTTTGTGCCATACCTGTATTAAGTTCAAGCCCTGGAATGATGAGGGCTTTTGCTCCA	2496
OY	2608	GAGCAGCTGTATAGTATCATGGGACATTTCTGGAAGAAAGCCTCCCAATGATGAGCTCTCGGAAAC	2667
Db	2497	GAGCCAGCTGCATCATATGAGACATTTCCGAGAAAGACCTTCCAAATGATGAGCTCTCGGAAAT	2556
OY	2668	GTGGCTGTGAATGTGTGTGAACAGTACCTTTAGCCGAGGTGACATGGGACCCAGTACCTCTG	2727
Db	2557	GTGGCTGTCAGTGTGTGTGAACAGACCTTTGGCAGGGGACACTGGGACCCCTGTACTCTCC	2616
OY	2728	AAAAGCATCCAGGACACCTTACAAAGGCTATGGAATTTCTATTTGGAAGACCAGAGTTCA	2787
Db	2617	AAGAGTGTCCAGAGACATTTCAAAGGCTTACCGGATTTTACTCTGGAAGGCTCAGAGCTCA	2676
OY	2788	TCTTAAAAAACAAGCGTCACTTGAAGAAAAGATCCCACTTCCAAAGGAGGAAGACT	2847
Db	2677	TCTTAAAAAACAAGCGCACATTTGAAGAAAGATCTCACCTTCCAGGGCAGGAAGACT	2736
OY	2848	CATGCGATGTTGCCGGGGCTAGAGGCCCTTTAGSCACTTACACTGAATGTCCGAGTGTC	2907
Db	2737	CACGGCATGTCTCCAGGGCTGCACCTTACAGTCACTATGTCTTCAATGTCCAGTGTGTC	2796
OY	2908	AATGGAAAAGGGGAGGCGCCAGCCAGCCCTTGAACAGAGTCTTTTAATCTCCAGAAAGAGTC	2967
Db	2797	AATGGAAAAGGGGAGGCGCCAGCCAGCCGACAGAGGCTTCCATATCTCCAGAGGAGTC	2856
OY	2968	CCCGATGTCCTCTCGTCTTTGAAGATGTGTAATCCAAACATGGACTGCTCTACCTTGGAA	3027
Db	2857	CCTAGTGTCTCCTCACTCTTTGAAGATGTATCTTACATGGACTGCTCTACCTTGGAA	2916
OY	3028	TGGATTCACCGAGGCCACCCGAATGSGACTTTTGCACAGATACACCTTAAAGTATCAGCA	3087
Db	2917	TGGGACCTTCCAGGCCACCCGAATGATGTCTGACTGAATACATCTTAAATATCAGGCA	2976
OY	3088	ATTAAACAGCACACATGAATTAAGGCCCTCTGTGTAATTTGAAATTTCTGCAACAGACA	3147
Db	2977	ATTATATACACACACAGACTAGGCCCTCTGTGTAATTTAAAAATTTCCGCAACAGACA	3036
OY	3148	CGGTGGAATTTAAAAATTTTAATTTTCAGCACTCGATATAGCTTTAATTTCTATGACAA	3207
Db	3037	CGGTGGAATTTAAAAATTTTAATTTTCAGCACTCGATCAAGATCTTCTTATATGACAA	3096
OY	3208	ACATCAGCAGGATCAGAAAGTCAAAATTCAGAGGAAGCAGTACACACTGTGATGAA---	3264
Db	3097	ACATCAGTGGGATCGGGCAGTCAAGTACAGAGGAAGCAATPAACACTGTGTGAGGAAGT	3156
OY	3265	-----GCTGTATTTCTTCAACTGTATGAGTGAAGCAAAAGTTCAAGCTGTAAATACC	3318
Db	3157	AAGAAGGCGGTGATTTCTTCAACTGATGTAGGTGACGCA-----	3197
OY	3319	AGGATCAGCAATCTTATCTGTGACAGCTGCTGAGACCTTATGCCAATATATGTTGGGAATAT	3378
Db	3198	-----	3197
OY	3379	GAGGAGCCAGAGCATGTGAATTTATGTGAATATGTGTGAAGCAGGCAAGAAAGAA	3438
Db	3198	-----	3197
OY	3439	TGGAAGAAAAGAAATGTAAATGTTCTCGAGACTTCTTTGGTTTAAAGGCTTAATGCA	3498
Db	3198	-----	3197
OY	3499	GGACAGCATACAAAGTTCGAGTGTGCTGTGGGGGACTCTGGTTTTGTGATTTCAAG	3558

D	b		3198		-----	3297	
Oy		3559	GATGTGTTTGAAGACAGGCCCCAGCGATTGGCAAAACCCTGGATGATATTGCACCTCAGGCG			3618	
D	b	3198	-----	AGCAATGGCAAGTCGGCAAGTGATATTGGACCCAGGC		3237	
Oy		3619	TGGTTCAATGGTCTCATGTGTGCTGTTGCTCTCTCTTAATTTTGGATGTTGTTGC			3678	
D	b	3238	TGGTTCAATGGTCTTAATGTGTGCTGTTGCTCTCTCATCTTAATTTTGGTAAATGCTTTGC			3297	
Oy		3679	TTTCATCAGAAAACAAGGCTGTAAATATTCAGTTAAGAAAAAGAAGATGCCATGCT			3738	
D	b	3298	TTTCATCAGAAAACAAGGCTGTAAATATTCAGTTAAGAAAAAGAAGATGCTCACGCA			3357	
Oy		3739	GACCTTGAATCCAGCCTATGAAGAAGATGATGCGCATTTGGAGAAATCAAGATGCA			3798	
D	b	3358	GACCTTGAATCCAGCCTATGAAGAAGATGATGCGCATTTGGAGAAATATGATGCA			3417	
Oy		3799	GAAGACCAACAAGCTTTGAAAAAAGAAAGTCSAAGCTCTTCAGACAGACTGTGAAAAA			3858	
D	b	3418	GAAATATCAACAAGCTTTGAAAAAAGGAAGTCSAACCTTCAGACAGACTGTGAAAAA			3477	
Oy		3859	GAAGATAGTGAACAAGCCTTAGTTACTATGAGAAAGGGGTTAATGSCCAGTTCAATGAG			3918	
D	b	3478	GAAGATAGTGAACAAGCCTTAGTTACTATGAGAAAGGGGTTAATGSCCAGTTCAATGAG			3537	
Oy		3919	GATGGCTCTTTATTTAGACAAATACAGTGTAAAGAAAGAAAGACCGGCTGAAGAAAC			3978	
D	b	3538	GATGGCTCTTTATTTAGACAAATACAGTGTAAAGAAAGAAAGACCGGGAAT			3597	
Oy		3979	GAAGCTCAGAGGACCTTCTCCTGTACAGCCATGAATTCCTTTGTTAA-TTTTTAG			4037	
D	b	3598	GAAGCTCAGAGGACCTTCTCCTGTACAGCCATGAATTCCTTTGTTAAAGCTTTAAG			3657	
Oy		4038	CTCAAAGCCAATATTCATTTCTTGAAGTTTATCTTAAGCTCTTGTGTAGCCCT			4097	
D	b	3658	CTCTGTCCCAATGTCCCATCTCTCTGGAATGGTTTCTTGAAAC- - - TTGTATCTCT			3713	
Oy		4098	CTCATCTATGAACATATGGGTAGAGATATTTTC			4134	
D	b	3714	CTCATCTATGAACATATGGGTAGAGATATTTTC			3750	
RESULT 10							
BC055053			4944 bp	mRNA	linear	ROD 08-OCT-2003	
LOCUS		Mus musculus RIKEN cDNA C130076007 gene,		mRNA (cDNA clone MGC:62892			
DEFINITION		IMAGE:649305?), complete cds.					
ACCESSION		BC055053					
VERSION		BC055053.1		GI:32822811			
KEYWORDS		MGC.					
SOURCE		Mus musculus (house mouse)					
ORGANISM							
REFERENCE							
AUTHORS							
		Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klauniger,R.D., Collins,F.S., Wagner,L., Sherman,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buelow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.T., Wang,J., Hsieh,F., DiChicento,L., Marusina,K., Farmer,A.A., Rubin,G.W., Hong,L., Stapleton,M., Soares,M.B., Donald,M.F., Casavant,T.L., Schreier,T.E., Brownstein,M.J., Udell,T.B., Toshiyuki,S., Carinci,P., Prange,C., Raha,S.S., Loggellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Boeck,S.A., McEwen,P.J., McNernan,K.J., Malek,U.A., Gunaratne,P.H., Richards,S., Woolley,K.C., Hale,S., Garcia,A.M., Gay,L.U., Huylk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,					

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Db	505	GTGCATCTGCAGAGGAACGAGCGTGGAGCGTCGCTCCAAATTAACATTTGTTCGCCCATC	564
QY	540	CAGATACCACTATGTGTGAGCAAAAGAAAACTTGAACCAATCACTTCCAAAGTGTCACTC	599
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QY	600	TTTAGTACTTCCCTGACAGACCCCAATTGGATTACACCACTATTAATTTTGGATGGA	659
Db	625	ATTAGTACTTCCATGTATGAGCCCTCGAATTGATTACTCCGGCCATTAATATTTTGGATGA	684
QY	660	TAATTCCTTTCAAAAGACTTCCAAAGTGAGAGAGTTTCTCAAGTTTGAATGGGGACT	719
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QY	720	TTAATTTTCCATGTCTCTCCAGAGAGACCCCGGAGAGACTATATCTGTATATGTATAT	779
Db	745	TTACTCTTCCATGTCTCTCCAGAGAGACCCCGTGAAGACTATATCTGTATATGTATAT	804
QY	780	TAATCATCTCAAAACCATATACAGACAGAAACCACTATTTCTGTGAAGGTGATTTCACTGA	839
Db	805	TAATCAGACTCAAAACCATATACAGACAGAAACCACTATTTCTTTGAAGGTGATTTCACTGA	864
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QY	900	AAGTAGAGAGAGGCGACCAACAATTTTAACTCCAGAAAGCAATGCAAGTAAACAAGAGA	959
Db	925	TAGTAAAGAGAGGCGCCCAACGTTTCTTACTCCAGAGGCAATGAAACCAACAAGAGA	984
QY	960	ATTAGAGAGAAATGTCTTTCACTGAGATGATTCAGAGAGACTGCTACCCCAATTA	1019
Db	985	ATTAGAGAGAAACGTGCTTTGCTGTGATGATTCAGAGAGACTGCTACCCCAATTA	1044
QY	1020	TTACTGGGCAAAAGAAATGGAATGTAATCTTCCAAAACAGACAGTTTATTAAGACTTTGA	1079
Db	1045	TTACTGGGATCAAAAGAAAGAGAAATGCTTCCGCGCAACGGAACATTTATCGGAACCTTAA	1104
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QY	1200	CTGATCAACAGCCCTCAAAATCTTTGTGCTGTCTCCAGAGAGAGATGGGACTTGAATCTG	1259
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QY	1260	CAGACTATATGGCAACCCCAAAACCGAAGATTAGCTGTATTAACAATGGAGTCCCAATGA	1319
Db	1285	CAGACTATATGGCAACCCGAAACCGAAGATTAGCTGTATTAACAATGGAGTCCCAATGA	1344
QY	1320	AATTGCCCTGTATGACCCCGAGGAGAAAAATGATGGCATACCAATTAATTTTCAAAATG	1379
Db	1345	AATTGCTCTCGATGACCCCGAGGAGAAAAATGATGGCATACCAATTAATTTTCAAAATG	1404
QY	1380	TCAAGAAAGATTAAGTGCATATATCAAGTGCATATGCTCTTAATGATATGATATTTACT	1439
Db	1405	TCAAAGAAAGCTCAAGTGGGTTTATCAAGTGCATATGCTCTTAACAATATGATATTTACT	1464
QY	1440	GGCAAGCGATTTGTAATATGTGTGTGGTGGAGCACAGAAATCCCAACCGGAAACAC	1499
Db	1465	ACCAATATGATTTGTAATATGTGTGTGGTGGAGCACAGAAATCCCAACCGGAAACAC	1524
QY	1500	ACTTACCAAGTCACTTGCAGAAACAGGCTGTCTTTAATAGCTGTGCTTTTGGGCTCTCC	1559
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QY	1560	TCCTCCCAACATCGATGTGTTTAAAGAGCTAAAGAAAGTCTCTTCAATGAAGATTTTA	1619

Db	1585	TATGCGTACCATTCGATGGTTTAAAGCCACTAAAGAAAGGCGTCTTCATGAAACATTTA	1644
Qy	1620	TGTTTTCATGAAAATGGAACCTTTGGAATTCAAAAGATGCTACATGCATCGTTAAAGAAAT	1679
Db	1645	TGTTTTGCATGATTAATGGAACATT-----AGMAAT	1674
Qy	1680	TCCTGTGGCCCCAAAGAACGCTAACAGGAACCTTATAGCGTGGTTGGCAAGAAATAAATAGG	1739
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Qy	1770	CGAATATGCAGTTGTGCAAAGAGGAGCATGTGTCTCTTTGAATGCAAAGTGAACATGA	1829
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Qy	1830	TCACACCTTATCCCTCCACTGCTCGTGGCTGGAAGAGCAACAGGGAACTGGCCAGTGTGA	1889
Db	1855	CCACACCTTATATCCCACTTATATGTGCTGAAGAGCAATGAGAGCTGCCCAATGATGA	1914
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Qy	1950	GACCTTACGCTGTGTGGCCAAACACACTCTGAGACAGCGTCTCGGCCAGCGCTGTGCTTAG	2009
Db	1975	AACTTACACGCTGTGCGGCCAAACAAACGCTGAGCAGTGTGCGCCAGCGCTGTGCTCAG	2034
Qy	2010	CGTTGTGCTCTTACTCCAACTCCAGCTCCCGTTTAAAGATGTCCTCCAAATCTCCCTTTGA	2069
Db	2035	GGTGTGCGCTCTTACTCCAACTCCAGCGCCCATTTAGATGATGCCGAATCTCCCTTTGA	2094
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Qy	2130	CAACATATGCCCCCATTTACAAAATTCATCATCGAATATGAAATGCAATGCAACAGCCAGG	2189
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Qy	2190	GCTGTGGGACACCAAACTGAAGTTTCTGGAAACAACAACACAGCCCAAGCTGAAGCTGTC	2249
Db	2215	GCTGTGGGACACCAAGGCTGAAGTTTCTGGAAACAACAACACAGCCCAAGCTGAAGCTGTC	2274
Qy	2250	TCCTTATGTAACACTACTCCTTCCGCGGTGAATGGACAGTGAACGCAATTTGGGAAAGACTTGC	2309
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Qy	2310	CAGCGAGGCGTCTGACAGTATTTGACGAAAGCTCTGAAACCAAGATTAACACCCACAGC	2369
Db	2335	GAGCGAGGCAATCCGAGCAGTATCTTTACAAAAGCCGACAGAACAGATCAGAAATCCCAATGCGC	2394
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Db	2575	AACTTTGTTCATCTCTGATCAAAAGTTCAAGCTCTGATATGATGTGGGCTTTTGCACAGA	2634
Qy	2610	GCGAGCTGTATGTCATGGGCAATTCCTGGAAGACCTCCCAATGGTGGCTCTCGGAACGT	2669


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ORIGIN

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Query Match      59.7%; Score 2468.4; DB 10; Length 5608;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 3269; Conservative 0; Mismatches 466; Indels 431; Gaps 9;

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QY 1900 TATGCTACATGATGATGATTTAAAGGACATTAAGAGAGCGCTTCTCATGAAGACATTTA
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RESULT 13

GENRCAM 3943 bp mRNA linear VRT 23-JUL-1991
 LOCUS Chiken mRNA for neuronal transmembrane protein Nr-CAM, ng-CAM
 DEFINITION related.

ACCESSION X58482
 VERSION X58482.1 GI:63706
 KEYWORDS cell adhesion molecule; neuron-glia cell adhesion molecule.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1
 Grunet, M., Mauro, V., Burgoon, M.P., Edelman, G.M. and Cunningham, B.A.
 Structure of a new nervous system glycoprotein, Nr-CAM, and its
 relationship to subgroups of neural cell adhesion molecules
 J. Cell Biol. 113 (6), 1399-1412 (1991)
 MEDLINE 91258407
 PUBMED 2045418
 REFERENCE 2 (bases 1 to 3943)
 AUTHORS Mauro, V.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-1991) V. Mauro, The Rockefeller University, 1230
 York Avenue, New York NY 10021, USA

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ORIGIN

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 VERSION AR177825.1 GI:17920180
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 ORGANISM
 Unknown.
 REFERENCES
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 AUTHORS Phillips, G., Cunningham, B. A. and Crossin, K. L.
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 Phasianinae; Gallus
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 AUTHORS Volkmer,H., Haseel,B., Wolff,J.M., Frank,R. and Rathjen,F.G.
 TITLE Structure of the axonal surface recognition molecule neurofascin
 and its relationship to a neural subgroup of the immunoglobulin
 superfamily
 JOURNAL J. Cell Biol. 118 (1), 149-161 (1992)
 MEDLINE 92317154
 PUBMED 1377696
 REFERENCE 2 (bases 1 to 4041)
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 TITLE Direct Submision
 JOURNAL Submitted (19-MAR-1992) H. Volkmer, Zentrum fuer Molekulare
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 Job time : 15702 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	2236	54.1	3943	4	US-08-506-2968-27 Sequence 27, App1
3	471.2	11.4	7647	4	US-09-566-921-75 Sequence 75, App1
4	405.8	9.8	3783	4	US-08-506-2968-20 Sequence 20, App1
5	351	8.5	3774	2	US-08-341-8438-1 Sequence 1, App1
6	351	8.5	3774	2	US-08-427-4978-1 Sequence 1, App1
7	351	8.5	3774	2	US-08-427-4978-2 Sequence 2, App1
8	347	8.4	3888	4	US-08-506-2968-13 Sequence 13, App1
9	316.2	7.6	3189	2	US-08-427-4978-3 Sequence 3, App1
10	228.8	5.5	2600	2	US-08-427-4978-4 Sequence 4, App1
11	157.4	3.8	3991	4	US-08-506-2968-3 Sequence 3, App1
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ALIGNMENTS

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; Sequence 724, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Funness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 724
; LENGTH: 6384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 201395.4
US-09-976-594-724

Query Match      78.2%; Score 3233.6; DB 4; Length 6384;
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Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;

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         637  CTTGCAAGATATATAGTCACTGAAGTCACTTGAATCCAAATCTTGAAGACTTG 696
QY      181 CTGTCCAGATGATATAGTCACTGAAGTCACTTGAATCCAAATCTTGAAGACTTG 240
         241  GTACGCTTCACACATACCAAGTCTCCAAAGTTTACATATATGACCTCGGAG 300
         697  GTACGCTTCACACATACCAAGTCTCCAAAGTTTACATATATGACCTCGGAG 756
QY      301 AATATTGTATCACTGTGAAGCAAGGAAAGCCGCCCAAGCTTTCTGACCCGT 360
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Qy 361 AATGGAGCTCATTTTGAACATCGATTAAGAAGCCCTGTGTCACCATGAAGCCTGGACACAGA 420
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Qy 481 TGTACAGCAAGGAACGAAGCGGAGCTGCACTTTCTAATPACATTTGTTCGCGCCATCC 540
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TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3943 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 33..3839
 US-08-506-296B-27

Query Match 54.1%; Score 2236; DB 4; Length 3943;
 Best Local Similarity 73.7%; Pired. No. 0;
 Matches 2916; Conservative 0; Mismatches 945; Indels 93; Gaps 2;

QY 98 CAGCAGAGTAACTAATGACAGCTTAAATAATGCGGAAAGAGCGCTTATCTGCGG 157
 DB 1 CAAGAGTGATTTAATGTAAGAGCTTAATCATGTAAGAGAGAGCATATCTGCA 60
 QY 158 GAGAGTGCCCTGATTTCTTCTGTCGCAAGATGATGATGATGATGATGATGATG 217
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RESULT 3
 US-09-566-921-75
 ; Sequence 75, Application US/09566921
 ; Patent No. 668288
 ; GENERAL INFORMATION:
 ; APPLICANT: Loxing, Jeanne F.
 ; APPLICANT: Tingley, Debora W.
 ; APPLICANT: Edwards, Carla M.

QY 2103 TGAAGTGTATGAGACCCAGGCGATGACAAATATGCCCCCATATACAAAATTCATCATCA 2162
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 QY 3063 AGAGTAACTTAAAGTATCAAGCAATTAACAGACACATGATTAAGGAGGAGGAGGAGG 3122
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 QY 3123 TTTGAAATTT--CTGCGCAACAGACAGGCTGATTTAAATTTAAATTTTAAATTTGAGC 3179
 DB 3220 TATTAACATTAACATCAATCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3279
 QY 3180 TGAATATAAGTTTATTTCTATGACAAACATCAGAGAGATCAGGAAGTCAAAATTAACGA 3239

DB 3280 CAAGTAAATTTCTACTTGAAGGCTTGGACCTTCAAGGAGGCTGTGAAAACCGATCAGGA 3339
 QY 3240 GGAA 3243
 DB 3340 GGAA 3343
 RESULT 4
 US-08-506-296B-20
 ; Sequence 20, Application US/08506296B
 ; Patent No. 6313265
 ; GENERAL INFORMATION:
 ; APPLICANT: Phillips, Greg
 ; APPLICANT: Cunningham, Bruce A.
 ; APPLICANT: Crossin, Kathryn L.
 ; TITLE OF INVENTION: NEGATIVE OUTGROWTH-PROMOTING POLYPEPTIDES
 ; TITLE OF INVENTION: CONTAINING FIBROBLAST TYPE III REPEATS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 77
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: The Scripps Research Institute
 ; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: U.S.
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/506,296B
 ; FILING DATE: 24-JUL-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Felling, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSKI 488.0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 554-2937
 ; TELEFAX: (619) 554-6312
 ; INFORMATION FOR SEO ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3783 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3783
 ; US-08-506-296B-20
 Query Match 9.8%; Score 405.8; DB 4; Length 3783;
 Best Local Similarity 46.8%; Pred. No. 1.2e-109;
 Matches 1771; Conservative 0; Mismatches 1887; Indels 123; Gaps 11;
 QY 229 TGGTACAGCTTCCAAACATCAACCCAGTCTCCAAAAGATTAATTAATTAATTAATTAATTA 298
 DB 92 TGGTACAGCTTCCAAACATCAACCCAGTCTCCAAAAGATTAATTAATTAATTAATTAATTA 151
 QY 229 AGAATATTTGTAATCAAGTGTGAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 358
 DB 152 ATGACATTAAGGCTGAATGTGAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 211
 QY 339 GATATGAGATCTATTTTATCAATGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 418
 DB 212 AAGATGAGATCACTTCAAAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 271
 QY 419 GAAGCTCATTAATTAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 475

Db 272 ATTCGGCTTCCTTCACATCGAAGGCAACAAGCTTTGCCCCAGAGGTTTCAGGGCATCT 331
Qy 476 ATCAGGTGACAGAAAGAAAGACCGGGAGCTGCAGTTTCTAATAATCTTTGTCGCCG 535
Db 332 ATCGCTGCTATGCGACAAATAGCTAGAACTGCCATGTCGATGATCCAGCTCTGG 391
Qy 536 CATCCAGATCACCATTGTGGACCAAGAAAATTGAAACCAATCACTTCAAGTGTG 595
Db 392 CCGAGGTCGCCCAAGTGGCCGAGAGAGACTGTAAACCTGTGGAAGTGGAGAGG 451
Qy 596 AGCTTTAGTACTTCCCTCGAAGCCCAATGGAATTCACACCTTAATATTTTGA 655
Db 452 AATCAGTACTGCTCTTCAACCTTCACCCAGTGCACCCCACTAGATCTACTGA 511
Qy 656 TGGATATTCCTTTCAAGACTTCCACAAGTGAAGAGTTTCTCAAGTTTGAATGGG 715
Db 512 TGAACGCAAGATTTTCGACATCAACAGATGAGGGGTGTCATGGGCCAGAAATGG 571
Qy 716 ACCCTATTTTTCCAATGTCCTCCAGAGAGACACCGGCAAGACTATATCTGTTATGCTA 775
Db 572 ACTTATATTTTGGCAATGTCTTACCTCAGACAAATCATTCAGACTACATCTGCAATGCC 631
Qy 776 GATTATATCTACTCAACCATACAGCAGAAAGCAACTATTTCTGGAAGTGAATTCAG 835
Db 632 ACTTCCCTGGTACCCGAGACCATCATTCAAAAGGAACCTATGACCTCCGGGTCAAGCCA 691
Qy 836 TGGATGAATTTGAATGACATATAGCTGTATATTGATGACACTGAGTTTATGTCGA 895
Db 692 CCAACGACATGATTGAC----- 709
Qy 896 AATCAAGTAGAGAGAGGCAACAATTTTAACTCCAGAAGCAATGCAATGAACAAG 955
Db 710 -----GGAAGCCAGTCTCTCTTTCCCAAAACTCCAGACGCCGCTGG 754
Qy 956 AGGAATTAAGAGAAATGTCTTCACTGAGTGCATTGCAAGAGACTGCTCAACCCAA 1015
Db 755 TAGCTTTCAGGGCCAGTATGATCTGAGAGTGCATTGCTGAGGATTCCTACACCCA 814
Qy 1016 TTATTTACTGGGCAAGAAAGATGGAATGCTACCCAAAACAGACAGTTTAAAGAACT 1075
Db 815 CCATCAAGTGGCTGCCACCCAGTACCAATGCAACAAGCGTGTATCTCAAAAACC 874
Qy 1076 TTGAGAAAACCTTGCAGATCATTCATGTTTCAGAAACAGACTCTGGAATTAACAATGA 1135
Db 875 ACAACAGAACCTTGCAGACTACTCAATGTGGGCAAGAGACAGATGCGAGTATACCTGCC 934
Qy 1136 TAGCAAAAATGCAATTAGAGCCCATCCACATACCAATTTCTGTTAGATTAAAGCGCTC 1195
Db 935 TTGCTGAGAACTCGTGGGCAAGTCCCGCATGCTTACTATGTTACTGGAAGCTGCC 994
Qy 1196 CATCTGGAATCAGACGCCCTCAAAAATCTGTGTGTCGCCAGAGAGATGGGACCTTGA 1255
Db 995 CATATTGGCTGCAAGAGCCCAAGCCCAATTTGTATGTTCTCAGAGAGACTGCCCGCTAG 1054
Qy 1256 TCTGCAGACTAATGSCAACCCCAACCCAGAAATGAGTGTGTTAAACAATGAGTCCAA 1315
Db 1055 ACTGCCAAATCCAGGGCAGGCCCAACAGAGATCACTTGGAGATCAACAGAAATGTCTA 1114
Qy 1316 TAGAAATTTGCCCTGATGACCCCAAGAAAATAGATGGCATACATTAATTTTTCAA 1375
Db 1115 TGGAGACGGTGAACAAGACACAAATGACCGGATGAGCAGGGGTCTGTGACTTGAATGA 1174
Qy 1376 ATGTTCAAGAAAGATCAAGTGCAGTATATCAAGTGCATGCTCTTATGATATGATATT 1435
Db 1175 AGGTGAGGCAACTGACAAATGTGACCAAGTGTAGAGCCGCAACGACAGGGCTCC 1234
Qy 1436 TACTGCAACGCAATTTGTAATGTGTGGCTGAGCACACGAATCTCAACCTGCA 1495
Db 1235 TGTACCAATGCTTCAATTTATGTTGTCCAGCTGCAGCAGAGATCTTAAACAAAAGACA 1294
Qy 1496 ACACACTTACAGGTCATTGCAACAGGCTGCTTACTAGACTGTGCTTTGGGT 1555

Db 1295 ATCAGACATATACATGACATGAGGGCAGTACTGCTTACTTCTGTGCAAGCCTTTGAG 1354
Qy 1556 CTCCTCTCCCAACCATGAGTGTGTTAAAGAGCTTAAAGAAAGTCTCTTCAATGAAGATA 1615
Db 1355 CTCCTGTTCCAGATGTCAGTGTGCTGATGTAAAGAAAGAACCAAGTGTCTTCAAGATGAAC 1414
Qy 1616 TTTATGTTTACATGAAAATGGAACCTTTGGAATCAAAAGATGTACATGATCGTTAAAG 1675
Db 1415 GATTTTCCCTATGCCAATGGAACGTGACATGAGACCTCCAGGCCAATGACACTG 1474
Qy 1676 AATTCCTGTGGCCCAAAAGACATGACAGAACTTAAGCTGTGTCGAAGAAATTAAT 1735
Db 1475 GACGCTATTTCTGCGAGGCTGCATTAAGACAGAACTATGTAATTTGCTTACCTTAC 1534
Qy 1736 TAGGATGCAAAAGATGAAGTTCACTTACAGCCCAATATGCAAGTTGTGCAAAAGAGGA 1795
Db 1535 AGGTTAAAGAAACCAACGATCACAAGGGGCCCCGAGGCAATTTGAAAGAAAGGTG 1594
Qy 1796 GCATGTTCTTTGATGATGCAAAAGTGAACATGATCACACTTATCCCTCACTGTCTGT 1855
Db 1595 CAGGGTGAATTCACGTGCGAGGCTCTTTGACCTCTTTTGAGGGCCAGACATCACTT 1654
Qy 1856 GGC-----TGAAGACAAAGAGAACTGCCCCAGATGATGAAGTTCACTGTGACA 1906
Db 1655 GGCCTGAGATGGAAGAGACCTTACAGAACCTGGGGAAGTGAATTTTATTAAG 1714
Qy 1907 AGGATCATCTAGTGTGACTGATGTCAGTGAAGTGAAGGAGGACTTACAGTGTG 1966
Db 1715 ATGGAAATCTAGTATCCAGAGCTTGAATCAGTGAACAGGCAACTTCAAGTTGTG 1774
Qy 1967 CCACACCACTCTGAGACAGCTCTCCGCAAGCTGTGCTTATGCTTGTCTCTACTC 2026
Db 1775 CCAGCATGAACTGATGAGGTGAGAGCAGGCAACACTCTTATGTTGGGAGACCCTG 1834
Qy 2027 CAATCAGCTCCGCTTATGATGTCCTCAATCTCTCTTGAATTAAGTGAAGATC 2086
Db 1835 GGCAGTGTCTTACCTGGA- GCTGTGCAAGCCCACTGTGGAAGCAAGCA----- 1886
Qy 2087 AACTTGACAAAAGTTCAGCTGTCATGAGACCCAGGAGATGACAAACATAGCCCATTA 2146
Db 1887 -----GTTGACCTTGTGTAAGTCCCTGTGAGAGACCAACTCTCCATTG 1933
Qy 2147 CAAAATTCATCTGCAATATGAAAGATGCAATGCAACAGGCTGTGCAACCAAA 2206
Db 1934 AGAAGATGACATTAATTTGAGACAAAGAAATGCTCTGGAATATGTTCACTG 1993
Qy 2207 CTGAAGTTTCTGGAACAAGACCAAGCCAGCTGAACCTGTCTCTTACGTGAACCTACT 2266
Db 1994 GCAGGTGCAAGAAATGAGACTTCTTACTTACCTTCAAGCTGTCTCTTATGTCCACTCA 2053
Qy 2267 CTTCCGCGTATGTCAGTGAACAGCATTTGGGAAGCTTGGCCAGAGGCTGTGAGC 2326
Db 2054 CTTTTCGGGTCACTGCCATTAACAAATATGTCCTGAGAAACCCAGCCCTGTCTTGAGA 2113
Qy 2327 AGTATTTGAAGAAAGCTCAGAACCAATTAACCCCAAGCTGTGGAAGACTGGAT 2386
Db 2114 GTGTGTCAACCTGAGGAGGCCCAAGAAAGAACTGTGATGTGAAGGGAGAGGA 2173
Qy 2387 CAGAGCTGATTAATTTGAGATTAAGTGAAGCCCTTGAATGTTTCAATTTATGAGC 2446
Db 2174 ATGAGACCAACAAATATGTCATCAATGAAAGCCCTTGTGATGATGGAATGAGCC 2233
Qy 2447 CAGGCTTCAGTACAAAGTTAGCTGGGCCAGAAAGATGTGATGATGAATGACATCTG 2506
Db 2234 CCAAGATTCAGTACCTGTACATGATGAGCTTCCAGAGGCAAGCAGAGAAAC 2293
Qy 2507 TGTGTTGCAATGATTAATTAATTTGTTCTCAGACAGCAACCTTTGTTCAATAC 2566
Db 2294 AGACGCTG---AGCAACCTTTCTGTGTGTCTTAACATTTCACTTTGCTTATG 2350
Qy 2567 TGATCAAAAGTCAAGCCCTGAATGACATGAGGTTTCCCGGAGCAGCTGTATGATG 2626
Db 2351 AGATCAAAAGTCAAGCAGTGAACCAACAGGGCAAGGGCCCTGAGCCCAAGTCAACATTTG 2410

2627 GACATCTGAGAGAGACCTCCCAATGAGTGGCTCTGGGAAACGTCGTGTAATGTGTGA 2686
2411 GCTATTCAGAGGAGAGACCTACCCCAAGTGAAGCTTAACTGTAAGACATCAATCTTCA 2470
2687 ACAGTACCTTGAAGGAGTGCATCTGGGAAACCACTGTAAGACATCCGAGACACC 2746
2471 ACTCAAGTACTGTGTCTGAGGTGAGGCTGTGAGCTTGGCCAGGTTAAAGGCCACCC 2530
2747 TACAGGCTATGAGATTTACTATTTGGAAGACCAAGTTCATTTAAAGAAACAGACGTC 2806
2531 TCAGAGGATACATGTAACATCTGTGAGAGGCGAGAGAGAAAGCACAGACAGAGG 2590
2807 ACATGAGAAAAAAGTCTCACTTCAAGGCGAGAGAGTCCAGTGTCTCCGAGG 2866
2591 AATTCACAAAAGCCACATAGTGTACCTGCAAAATCCACAGTGCATCTCAAGTGT 2650
2867 TAGAGCCCTTGAAGCACTACACATGATGTCCGAGTGTCAATGGGAAAAGGAGGCGC 2926
2651 TGGGCCCTTACAGCTCTTACATGTGAGGTAAGGCTTAAATGGGCGGAGCTTGGGCG 2710
2927 CAGCCAGCCCTGACAGAGTCTTAAATCTCCAGAGAGTCCCAAGTGTCTCTCTT 2986
2711 CTGCGAG--TGATGAGACCTTCAGACCCAGAGGAGTGTCTGCGCACCTGAGGCA 2767
2987 TGAAGATTGGAATCCACACTGAGCTCTCTCACTTGAATGGATCCAGAGGCGACC 3046
2768 TACACTGAGTGTCTGAGTGAACATGATGTCTGCTGCTGCTGAGCGCCACCTAGACC 2827
3047 CGAATGGCAATTTTGAAGAGTACACCTTAAAGTATGAGCCATTAACAGACATGAAT 3106
2828 AATATGAGTGTCTCACTGCTGCTGCTCTTACATCCCGTGAAGGAGAAAGCAAG 2887
3107 TAGGCCCTGTGTGATTTGAAATTCCTGCAACAGACAGCGTGTGAATTTAAAT 3166
2888 A-----GCAGTGTCTTCAACCTTCCGAGCCAGAACCTCCGACATCATATCTGA 2938
3167 TAAATTTGCACTGATATTAAGTTTATTTATGACAAACATCAGCAGATCAGAA 3226
2939 CCAACTCAACCTGATCTTACATACCTGCTTCAAGCTTCAAGCCACCAACAGGAG 2998
3227 GTCAATATCAGAGAGAGAGTAACTGATGATGATGATGATGATGATGATGATGAT 3286
2999 GTCTGTGTGAGGCACTGTGCGGAGAGGAGGACCAATGCGCTGTTGGAGACGAT 3058
3287 TAGGTGAGGCAAGTCAAGCTGTAAATCCAGATCAGCAATCTTACTGCTGACGCTG 3346
3059 TTGGCAACATCTCAGCCAGCAGGAGTGAAC-----TACAGCGTGTCTC 3104
3347 CTGAGACCTATGCAATATCAGTTGGAATATGAGGAGCAAGCAGATGAACTTTATG 3406
3105 CTGGGTCTCTCGAAGAGGCGAGT--GCAATTCAGGTTCCATATCTTGT--TCAAGCCT 3160
3407 TGAATATGATGTGAGCAGCAGCAAGAAAGATGAGAAAGAAATTTGTAATGTTCTC 3466
3161 TACCAAGAGGAGAGAGAGGCGCTGATCAACAGCTCAGCTCAGTATGTAGTACAAAT 3220
3467 GAGCTTCTTTGGGTTAAAGGCTTAATGCTCAGAGAAACAGATCAAAAGTTGAGTGGTG 3526
3221 AGAGCTCTACACACATGGAACCTCAGCTCAGACCAAAATATGAGATCAGCTATTA 3280
3527 CTGTGGGAGCTCTGTGTTTGTGAGTTCAGAGATGTTTGAAGACAGGCGAGCATG 3586
3281 AGAGAGAGGCTCTCTGCAACATCTGAGATGTAAGACATAGGAGCTGTGCGAG 3340
3587 CAGCCGAGAGTGAATATGCAACTCAGGCTGTGTCAATGTGTCTGATGTGTGTTG 3646
3341 TTTCTACTACAGGAGCTTTGCTCGAGGCGGTGTTCAATGCGCTTGTAGGCGATCA 3400
3647 CTCTCTTAATCTTAATTTTGTGATGTTTGTCTTCAATCAGAGAAACAAAGGTGTAAAT 3706
3401 TTTCTTTGCTCTCTCATCTGCTCATCTCTGCTTCAATCAACAGCAAGGCTGTGCAAT 3460

QY 3707 ATCCAGTTAAAGAAAAGAGATGCCCATGTGACCTTGAAAATCCAGCTATGAGAG 3766
DB 3461 ACTCAGTAGAGAGACAGAGAGACCTCAGGTGATTCGAGGCGCGCCATGAAAGAG 3520
QY 3767 ATGATGGACATTTGGAAGATCAGTGTGAGAGAGACCAAGCTTTGAAAAAGAA 3826
DB 3521 AGACCTTCGGCAGATACAGTCCCTGAGAGTGAATGAAAGAGAGGCTTTGGCAGA 3580
QY 3827 GTGCAACTCTTCAGACAGACTGTGAAAAAAGAAATGATGACGACAGCTAGTTGACT 3886
DB 3581 GCCAGCATCTCTCAACGAGAGACATCAACCCCTAGCAGTATGACAGCTGCTGAT 3640
QY 3887 ATGAGAAAGGAGTTAATGAGCAGTTCAATGAGATGCTCTTATTTGACAAATCAGT 3946
DB 3641 ATGGGGGAGGTGTGAGCGTCCAGTTCAATGAGATGCTCTTCAATGCGCCAGTACAGT 3700
QY 3947 GTTAAAGAGAAAGAGCCGCTGAAAGAAAGAAAGCTCAAGGCACTTCTCTGTCA 4006
DB 3701 GCAAGAAAGAAAGAGGAGGAGGAGGCAATGACAGTTCAAGGAGCTACTCTCTATCA 3760
QY 4007 A 4007
DB 3761 A 3761

RESULT 5
US-08-341-843B-1
Sequence 1, Application US/08341843B
Patent No. 5872225
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of L10M and
Patent No. 5872225
TITLE OF INVENTION: the Nucleotide Sequence
NUMBER OF INVENTION: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: Pay, Sharpe, Beall, Fagan,
STREET: 1100 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,843B
FILING DATE: No. 5872225ember 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3774
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

OY	2024	CTCCAACTCCAGCTCCCGTTTAAAGATATGCCAAATCCCTCCCTTGAAGCTTAAAGACAG	2033
Db	1835	CTGGGCGCGGT--GCCAGCGCTGGTGTCTTCGCCCTCGACCTCGTGAACCGAAGC-----	1887
OY	2084	ATCAACTTGAAGAAAGTGTACGCTGTATGGACCCGAGCGATGACAACAATAGCCCCA	2143
Db	1888	-----CAGTTGCCCGGTCTCTGGAGTCTTGAGAGAACCAATATGGTACAGTC	1933
OY	2144	TTACAAAATTCATCATCGAATATGGAATGCAATGCAATGCAACAGCCAGGCGTGTGGCAAC	2203
Db	1934	TTGAGAAATATGACATTTGAATTTTGAGGACAAGAAATAGCGCTGAATAATATGGTACAGTC	1993
OY	2204	AAACTGAAGTTTCTGGAACACAGACCAAGCCGAGCTGAGTGTCTCTTAACGTAACT	2265
Db	1994	TGGCGAAGTTTCCAGGGAAACAGACCTTACCACTCAAGCTGTGCGCTATGTGCCACT	2053
OY	2264	ACTCCCTTCCGCGTGAATGGCAGGAACAGCATTTGGGAAGAGCTGGCCAGCGGCGTCTG	2323
Db	2054	ACACCTTTAAGGTTTACTGCCATTAACAAATATGGCCCGGGAGACCCAGCCCGGTCTCTG	2113
OY	2324	AGCAGTATTTGACGAAAGCCTCAGAAACGATTAATAAACCCCAAGCTGTGGAAGACCTG	2383
Db	2114	AGACTGTGTCACACCTGAGGAGCGCCAGAGAAAGAACCTGTGTGATGTGAAGGGGGAAG	2173
OY	2384	GATCAGAGCCTGATTAATTTGGAGATTACGTGGAAAGCCTTGAATGTGTTTCAATTAATG	2443
Db	2174	GAAATGAAACACCAACATATATGTGCATCAAGTGAAGCCCTCCGCTGTGATGACCTGGAACG	2233
OY	2444	GAGCAGGCTTCAGTACAAAGTTAGCTGGCGCAGAAAGATGTGATGATGAATGGAACAT	2503
Db	2234	CCCCCAGGTTCAAGTACCGCGTGCAGTGGCGCTTCAGAGGACACAGAGGCGCTGGCAGG	2293
OY	2504	CTGTGTGTGTGGCAAAATGATATCAAAATTAATTTGTCTGAGGACGCAACCTTTGTTCCAT	2563
Db	2294	AGCAGATTGT---CAGCGACCCCTTCCGTGTGTGTCCAAACAGTCCACCTTGTGTCCT	2356
OY	2564	ACCTGATCAAAAGTTACGAGCCCTGAAATGACATAGGGGTTTGGCCCGAGCCAGCTGTATGCA	2623
Db	2351	ATGAGATCAAAAGTCCAGGCGCTCTCAACAGCCAGGGCAAGGAGACAGAGCCCGCAGGTCACTA	2410
OY	2624	TGGGCAATTTCTGGAGAAACCTCCCAATGTGTGGCTCTTGGGAAGTGGCTGTGAATGTGG	2683
Db	2411	TGCGGTACTCTGGAGAGGACTAACCCCGAGGCAATCCCTGAAGCTGGAAAGCATTTGMAATCC	2470
OY	2684	TGAACAGTACTTAGCCGAGGTGACATGGGACCCAGTACCTCTGAAAGAACATCCGAGGAC	2743
Db	2471	TCAATCTCAATGCGCGTGTCTGTCAATGTGGCGCGCGCTGTGACCTGGCCAGGTCAAGGCGC	2530
OY	2744	ACCTACAAAGCTATCGAATTTACTATTGGAAGACCCAGAGTTTCAATCTTAAGAAAGAACAGAC	2803
Db	2531	ACCTCCGGGATACAAATGTGACGTACTGGAAGGAGGCGACGTACAGAGAAAGCACAGCAAGA	2590
OY	2804	GTCACATTGAGAAAAAGATCCTCACCTTCCAAAGGACGAAGATCTCATGTGGATGTGGCCGG	2863
Db	2591	GACATATCACAAAAGACCATGTGTGTGTGGCCCGCCAGAACACACACAGTGTCAATCTCAATG	2650
OY	2864	GAGTAAAGACCTTTTAAAGCACTACACATGGAATGTCCAGTGTGTCAATGGGAAAGGGAGAG	2923
Db	2651	GCTTGGCGCCCTAATAGCTCTTCAACCTGGAAGGTGACAGGCTTTTAAGGGGAGAGATCG	2710
OY	2924	GCCGAGCCAGGCTGACAGAGTCTTTTAATCTCCAGAAAGAGATCCCATGTCTCTCCCTGT	2983
Db	2711	GGCCCGCGCAGC---GAGTTCACTTACAGCAACCCAGAGAGAGTGTCTGGCCACCCCGAAG	2767
OY	2984	CTTTGAGATTGTGATCAACAACCTGGAATCTCTCACTTTGGAAATGGGATCAACGAGCC	3043
Db	2768	CGTTGCACTTGAAGTGCAGTGTGAACAACAAGCTGTGCTGTGCGCTGGAGCGCCCATCTCA	2827
OY	3044	ACCGGAATGGGAATTTTGAACAGATACACCTTAAGATACAGCAATTAACAGACACATGT	3103
Db	2828	GCACAAAGGGGTGTCTACCGGCTAAGTGTCTCTTACACACCCCT-----GGATG	2878

QY	3104	AATTAGGCGCCCTGCTGATGATTGAAAATTCCTGCGCAACAAACACGCGGTGGACTTTAAAAA	3163
Dp	2879	AGGGGGGCAAGGGGCMACTGCTCTTCACTCTGGACCCCGAACTTCGGACACACACC	2938
QY	3164	ATTTAAATTCGACACTCGATATATAGTTTATTTCTATGCAAAACATTCACGAGATCAG	3223
Dp	2999	TGACCGATCTAGGCCCCACCTGGGGATACGGCTTCAGCTTCAGGCCACCAAGAGG	2998
QY	3224	GAACTCAAATTACAGAGAGACAGTAACACTGTGATGAACTGTGATTTCTCACCTG	3283
Dp	2999	GCCCT-----GGTGAAGCCATGTACGGAGAGAGCACTATAGGCTT	3041
QY	3284	ATGTAGGCGCAGCAAGTTCAAGCTGTAAATACAGAGATCAGCAATCTTACGTCTCAG	3343
Dp	3042	GCTGGGATCTCAGATTTTGGCAACATCTCAGCCACACGGGTGAAAACTACAGTGTCT	3101
QY	3344	CTGCTGAGACCTATGCAATATTCAGTTGGGAAATGAGGGACGAGCATGTGAACTT	3403
Dp	3102	CTCCTGGGTCCCAAGGAGGGCCAGT--GCAACTTCAGGTTCCATCTTGTTCAAAGCC	3159
QY	3404	ATGTTGAATATGTGTATGACGAGCAGCAAGAGATGAGAAAAGAAATGTAAATGTT	3463
Dp	3160	TTGGGAGAGAGAGGGGTGGGCTTCCCTTTCG-----CCACAGTATGTCAGTACA	3211
QY	3464	CTCGAGCTCTTGGGTAAAGGGGTAAATGCGAGAAACGATACAAAGTTGAGAGTT	3523
Dp	3212	ACCGAGTCTTACACGATGGGACCTGACGCTGACACTGACATCAGATCCACTTGT	3271
QY	3524	GTGCTGTGGGGACTCTGTTTGTGTGATTCAGAGATGTGTGTTGAGACAGGCCACGGA	3583
Dp	3272	TTAAGAGAGGATGTTCCGCGACCAATGGCTGTGAAGCAATGGCACAGGCCGTGA	3311
QY	3584	TGGCAGCGCGCAGGTGATATTGCAACTCAGGGCTGTTCATTGTGTGTGCTG	3643
Dp	3332	GG---CTCCCTCCGTGGCTTCCGCACTGAGGCTGTTCATCGGCTTGTGTAGTCCA	3388
QY	3644	TTGCTCTCTATCTTAATTTTGTGATTTGTTGCTTCACTCAGAAAGAAAGGGTGTG	3703
Dp	3389	TCATCTCTCTGCTCTGTGCTGCTCACTCTGCTTCACTCAAGCGACAGGGCGCGA	3448
QY	3704	AATATCCAGTTAAAGAAAGAGAGATGCCATGCTGACCTCGAATCCAGCTTATGAAG	3763
Dp	3449	AATATCTCAGTGAAGGATTAAGAGAGACACCGAGTGAATCTGAGGCCCGAATGAAG	3508
QY	3764	AAGATGATGGGACATTTGGAGATACAGTATGCAAGAACACACAGCCTTTGAAAAAG	3823
Dp	3509	ATGAGACCTTGGGAGAGTACAGTCCCTGAGAGATGACAAAGAGAAAGGCTTTGGCA	3568
QY	3824	GAAATCGAATCTCTTCAGACACAGACTGTGAAAAAAGAAATAGTACAGACCTTATGTG	3883
Dp	3569	GCACCCAGCCATCTCTCAACGGGAGCATCAAGCCCTCTGGGAGATGACAGCCTTGCCG	3628
QY	3884	ACTATGAGAAAGGGGTTAATGGCAGTTTCAATAGAGATGGCTCTTTATTTGACAAATACA	3943
Dp	3639	ATTATGGGGGAGGCTGATGTTCAATTTCAACAGAGATGTGTCTTATTTGGCCAGTACA	3688
QY	3944	GTGTTAAGAAAGAGAAAGAGCGGCTGAAGGAAACGAAGCTCAGAGGCATCTTCTCTG	4003
Dp	3689	GTGGCAAGAGAGAAAGAGGCGGACAGGGGCAATGACACTCAGGGGCCACTTCCCA	3748
QY	4004	TCAACGC 4010	
Dp	3749	TCAACCC 3755	

RESULT 6
US-08-427-497B-1
; Sequence 1, Application US/08427497E
; Patent No. 5969124
; GENERAL INFORMATION:
; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of L1CAM and

Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3774
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional
TITLE: testing of human L1CAM: an
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 1 to 3774
US-08-427-497E-1

Query Match 8.5%; Score 351; DB 2; Length 3774;
Best Local Similarity 46.2%; Pred. No. 2.2e-93;
Matches 1749; Conservative 0; Mismatches 1900; Indels 138; Gaps 12;

QY 239 TGGTACAGCTCCACATCAACCAAGTCTCCAAAGATTACATTATGACCTCGGG 298
DB 92 TGAATGAGCCACTGTCATCAACGAACAGTCTCCAGCGCGCTGTGTTCTCCACAG 151
QY 299 AGAATATTGTATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTGAGCC 358

DB 152 ATGACATCAAGCTCAAGTGTGAGGCCAGTGGCAAGCCGAAAGTGCAGTTCGGTGAACA 211
QY 359 GTAATGGAGCTCATTTTGAATCATGATTAAGACCTCTGTGTCACATGAA-----GCCTG 412
DB 212 GGGATGTGTCTCATTTCAAAACCAAGAAAGAGCTGGGTGTGACCGGTATCCAGTGGCCCC 271
QY 413 GCACAGAAACGCTCAATTAATTAATCATGAGCGAAAGGAAAGCTGAGACTATGAAAGAG 472
DB 272 ACTGTGCTCTTCAACCATACAGGGCAACACAGCACTTTGCTCAGAGGTTCCAGGGCA 331
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QY 533 GCCCATCCAGATCACCATTTGTGACCAAAAGAAACCTTGAACCAATCACTTCAAGTG 592
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QY 713 GGGACCTTATTTTTCATGTCCTCCAGAGAGACCCGCAAGATATATCTGTATG 772
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Qy      4004 TCAAGC 4010
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RESULT 8
us-08-506-296B-13

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/ Sequence 13, Application US/08506296B
/ Patent No. 6313265
/ GENERAL INFORMATION:
/ APPLICANT: Phillips, Greg
/ APPLICANT: Cunningham, Bruce A.
/ APPLICANT: Crossin, Kathryn L.
/ TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
/ TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
/ NUMBER OF SEQUENCES: 77
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: The Scripps Research Institute
/ STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
/ CITY: La Jolla
/ STATE: California
/ COUNTRY: U.S.
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/506,296B
/ FILING DATE: 24-JUL-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSRI 488.0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 554-2937
/ TELEFAX: (619) 554-6312
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3888 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 12..3773
/ US-08-506-296B-13

Query Match      8.4%; Score 347; DB 4; Length 3888;
Best Local Similarity 46.5%; Pred. No. 3.5e-92;
Matches 1762; Conservative 0; Mismatches 1875; Indels 150; Gaps 14;

Qy      239 TGGTACAGCTCCCAACATCAACAGTCTCCAAAAGATTATTAATGACCTCGGG 298
Db      103 TATGAGCGACCTGTCTATCAGGAACAGTCTTCCAGCGCGCTGTGCTTCCACAG 162
Qy      299 AGAATATGTAATCCAGTGTGAAGCCAAAGGAAACGCCCAAGCTTTCTGAGACC 358
Db      163 ATGACATCAGCTCAAGTGTGAGGCAAGTGCAGACCGAAGTGCAGTTCCCTGAGCA 222
Qy      359 GTAATGGGCACTATTTGACATGATTAAGACCTCTGTGACCATGAA-----GCCTG 412
Db      223 GGAATGTGTTCACATTCAAACCAAGAGAGCTGGGTGTGACCGTGTACAGTGGCCCC 282
Qy      413 GCACAGGAACGCTCAATTAATCATCATGAGGGAAGGAAAGCTGAGACCTTATGAGAG 472
Db      283 ACTTGGCTCTTCAACATCAAGGCAACAGCAACTTGTCTAGAGGTTCCAGGGCA 342
Qy      473 TCTATCAGTGTACAGCAAGAAAGAAAGCGGAGCTGCAAGTTCTTAATAATTTGTTGCC 532
Db      343 TCTACCGCTGCTTTCAGCAATTAAGCTGGGCAAGCCATGTCCATGAGATCCGGCTCA 402
Qy      533 GCCCATCAAGATCACCATTGTGTGACCAAGAAAGAAAGAAAGCTTGAACCATCACTTCAAGT 592
Db      403 TGGCGAGGGTCCCAAGTGGCCAAAGAGACAGTGAAGCCGTTGAGGTGAGAGANG 462

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2542 ACCCTGGGATATCAATGTAGCTA CTGAGGGAGGAGTCAAGAGACAGACAGACA 2601
2804 GTACATTTAGAAAAAGATCTCTCACTTCCAGGAGCAAGATCTATGTCATGTCGG 2863
2602 GACATATCCAAAGACCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2661
2864 GGTAGAGCCCTTTAGCCCTACACACTGATGTCCGAGTGTGCAATGGGAAAGGGAG 2923
2662 GCTTGGGGCTTATATCTTACCTTACCTTGAAGTGTGAGGCTTTAAAGGCGAGAT 2721
2924 GCCAGCCAGCCCTGACAGAGTCTTAAATCTTCAGAGAGAGTCCCAAGTCTCTCT 2983
2722 GGGCCGCGCAGC---GAGTTCACCTTCAGACCCAGAGGAGGTGCTGGCCACCC 2778
2984 CTTTGAAGATTGTGATCCAACTGAGCTCTCTCTCTTGTGATGGGATCCAGCCAG 3043
2779 CGTTGACCTGTAGTCCAGTGCAGACCAAGCTCTGCTGCTGCTGCTGCTGCTGCT 2838
3044 ACCGGAATGGCAATTTTGAAGAGTACCTTAAAGTATGAGCAATTAACAGACATG 3103
2839 GTCACACAGGCGGTGTCTACCGGTAGTGTCTCTCTACACACCCCTG-----G 2889
3104 AATTAGGCGCTGTGTAGATTGAAATTCCTGCCAACAAGACGCTGAGCTTTAAAAA 3163
2890 AGGGGGGCAAGGGGCAACTGTCTTCACTTCGGGAGCCCGAATTCGAGACACAGCC 2949
3164 ATTAAATTTCACTGATCCATTAATTTTATTTATTTATTTATTTATTTATTTATTT 3223
2950 TGAACCATTCAGCCCCCAGCTGGGTACCGGTTCAGCTTCAGGCGACACCAAGAG 3009
3224 GAAGTCAAAATTACAGAGAAAGCAGTAACAATGTGATGAGTGTATTTCTTCCACT 3283
3010 GCCCT-----GTTAAGCATCTGTACGGAAGAGAGGACATATGCTT 3052
3284 ATGTAGTGCAGGCAAAAGTTCAAGCTGTAAATACAGATTCAGCAATCTTATCTG 3343
3053 GTCTGGATCTCAGATTTTGGCAACATCTAGCCACAGCGGTGAAGAACTACAGTGT 3112
3344 CTGCTAGACCTATGCAATATGATGTTGGAAATATAGAGGACAGAGCATGTAATTT 3403
3113 CTCTGGGTCCCAAGAGGCGCAGT--GCACCTTAGGTTCCATATCTTGTTCAGAG 3170
3404 ATGTATATATGTGTAGCAGGAGCAAGAAAGATGAGAAAGAAATTTGTAATGTT 3463
3171 TTGGGAGAAAGAGGTGGGCTTCCCTTGC-----CCACGATATGACGTACA 3222
3464 CTCGAGCTTTTGGGTTAAAGGTCATATGTCAGGAAACAGATACAAAGTTGAGTT 3523
3223 ACCAGAGCTCTACAGCAGTGGGACTGCAAGCTGACACTGACATCAGATCCTTGT 3282
3524 GTGCTGTGGGAGCTGTGTTTGTAGATTCAGAGATGTGTTGAGACAGGCGCAGCA 3583
3283 TTAAAGAGAGGATGTTCCGACCAAAATGCTGTGAAGACCAATGACACAGGCGGT 3342
3584 TGGCAAGCGGAGTGTATTTGCAACTCAGGGCTGTTCATTTGCTGATGTGTGCTG 3643
3343 GGT---CCCTCTGCTGCTGTGCACTGAGGGCTGTTCATCGGCTTTGTGAGTGCA 3399
3644 TTGCTCTCTTATCTTAATTTTGTGATTTGTTTCAATCAGAGAAACAAAGGTGTA 3703
3400 TATCTCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3459
3704 AATATCAATTAAGAAAGAAAGAGATGCTTCACTGAAATCCAGCTTATTAAG 3763
3460 AATATCAATTAAGAAAGAAAGAGATGCTTCACTGAAATCCAGCTTATTAAG 3519
3764 AAGATATGAGCAATTTGAGAAATAGATGATGATGATGATGATGATGATGATGATG 3823
3520 A-----TGAACCTTCTGGGAGTACAGTACACAGAGAGAGGCTTTGGCA----- 3567
3824 GAAGTGAACCTCTTCAAGACAGACTGTGAAAAAAGATAGTGAACAAGCTTGTG 3883

3568 GCAGCCAGCCATCGCTCAACGGGAGCATCAAGCCCTGGGAGTGAAGACAGCTGGCG 3627
3884 ACTATGAGAGAGGGTTATGAGCAGTTCAATGAGATGAGCTCTTTATTTGGAATACA 3943
3628 ATTATGGGGGAGCGGTGATGTTTCACTTCAAGAGATGTTTCTTCAATTTGGCCAGT 3687
3944 GTGTAAAGAAAGAAAGAGCGGCTGAGAGAAAGCAAGCTCAGAGGACCTTCTCTG 4003
3688 GTGGCAAGAGAGAGAGAGGCGGAGGGGCAATGACAGCTCAGGGGCCACTTCCCCCA 3747
4004 TCAAGC 4010
3748 TCAACC 3754

RESULT 9
US-08-427-497E-3
Sequence 3, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
NUMBER OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427, 497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904, 991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3189
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
LIBRARY: StrataGene cDNA Library 936206
CLONE: 3.1
PUBLICATION INFORMATION:

AUTHORS: Hlavín, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 548 to 3736

US-08-427-497B-3

Query Match 7.6%; Score 316.2; DB 2; Length 3189;
Best Local Similarity 46.7%; Pred. No. 4.3e-83;
Matches 1411; Conservative 0; Mismatches 1533; Indels 75; Gaps 10;

QY 982 CTGGAGTGCATTGCAAGAGACTGCTTACCCCAATTTTATCTGGGCAAGAAATGGA 1041
DB 237 CTGGAGTGCATTGCAAGAGACTGCTTACCCCAATTTTATCTGGGCAAGAAATGGA 296
QY 1042 ATGCTACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1101
DB 297 CCCATGCCAGCTGACCGTGTACCTTACCAAGACCAAGAGAGAGAGAGAGAGAGAG 356
QY 1102 GTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1161
DB 357 GTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
QY 1162 CACCAATCACTTTCTGTGAGTTAAAGCGGCTCATTGATGACAGCCCTCAAAAT 1221
DB 417 CGGCAATCACTTTCTGTGAGTTAAAGCGGCTCATTGATGACAGCCCTCAAAAT 476
QY 1222 CTGTGCTGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1281
DB 477 CATCTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
QY 1282 CCCAGATTTAGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1341
DB 537 CCAGAGTCACTGTGAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
QY 1342 AGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1401
DB 597 TACCGATTTAGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
QY 1402 TATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1461
DB 657 ACCCAATTTAGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716
QY 1462 CTGGAGTGCATTGCAAGAGACTGCTTACCCCAATTTTATCTGGGCAAGAAATGGA 1521
DB 717 GTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 776
QY 1522 AGGCTGTCTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1581
DB 777 AGGCTGTCTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 836
QY 1582 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1641
DB 837 GACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896
QY 1642 TTGGAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1701
DB 897 CTGGAGTGCATTGCAAGAGACTGCTTACCCCAATTTTATCTGGGCAAGAAATGGA 956
QY 1702 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1761
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DB 1017 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
QY 1822 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1872

DB 1077 TCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
QY 1873 GAACTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1932
DB 1137 GAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1196
QY 1933 AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1992
DB 1197 GACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1256
QY 1993 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2052
DB 1257 AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
QY 2053 CCAATTCCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2112
DB 1316 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1355
QY 2113 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2172
DB 1356 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1415
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QY 2233 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2292
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QY 2293 ATTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2352
DB 1536 TATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1595
QY 2353 GATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2412
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DB 1656 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1715
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QY 2653 GTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2712
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QY 2713 GACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2772
DB 1953 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2012
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Db 2190 ACCCCAGAGGAGTGTGCTGGCCACCCCGAGGCGTTTCACTGAGTGCAGTGAACACC 2249
Qy 3013 TCTCTCACTTTGGATGGATTCACCGAGCCAGCCGATGGCATTTTGAACAGATACACC 3072
Db 2250 AGCTCTGCTGTGGCTGGACAGCCCGCACTACGACACAGGGGTGTCTACCCGGCTACG 2309
Qy 3073 TTTAATATATGCAATTAACAGACACATGATTAAGCCCTTGTGTATATTGAAAT 3132
Db 2310 CTCTCTTACACCCCTGTGATGAGGGGGCAAGGGGCAATGTCTTCAACTTTCGGGAC 2369
Qy 3133 CCTGCAACAAGACAGGTGATCTTAAATAATTTTAAATTTTGAAGTATTAAGTT 3192
Db 2370 CCGGAACCTTGGACAC---ACAACTGACCGATCTACAGCCCGCACTGGGGTACCGCTTC 2426
Qy 3193 TATTTCTATGCAAAATCATCAGAGGATCAGAAATCAATTAACAGAGGACAGTAA 3252
Db 2427 CAGCTTCAAGGCCACCAACAAAGAGGCCCTGTGAAGCATGTACGGGAAGGAGCACT 2486
Qy 3253 ACTGTGATGAGAGCTGTATTTCTTCACTGATGTAGTGTGACGCAAGTTCAAGCTGTA 3312
Db 2487 ATGG-----CCTTGTCTGGATCTCAGATTTTGGCAACATCT 2523
Qy 3313 AATACAGAGATCAGCAATCTTACTGTGACGTGCTGAGACCTATGCAATATCAGTTGG 3372
Db 2524 CAGCCACAGGGGTAAACTTAAGTGTCTCTCTGGGTCCCAAGAGAGGCCAAT--G 2581
Qy 3373 GAATATGAGGACACAGAGATGTAATTTTATGTTGAATATGATGTAGAGGACAGCA 3432
Db 2582 CAATTCAGGTTCAATCTTGTTCAAAGCTTGGGAGAAAGAAAGGTGGGGCTTCCCT 2641
Qy 3433 GAAAGATGAGAAAAGAAATTTGAATGTTCTTCGAGCTCTTGGGTAAAGGTCTTA 3492
Db 2642 TTGG-----CCACAGTATGTCACTCAACCAAGGCTCCCTACAGCAGTGGGACCTG 2693
Qy 3493 ATGCCAGAAACAGCATATCAAAAGTTGAGTTGGTGTGGGGGACCTGGTTTGTGAGT 3552
Db 2694 CAGCTTGAACCTGACTGACGATGATCCTTTTAAAGAGAGATGTTCCGGACCAAAAG 2753
Qy 3553 TCAGAGATGTGTTTGAACAGGCCCGACGATGAGGACCGGAGGTGATATTCAGT 3612
Db 2754 GCTGTAAAGCAATGAGCAGGCCGCGGTGAGG---CTCCCTCTGTGGCTTCGCACT 2810
Qy 3613 CAGGCTGTGTTATGTTGCTGATGTGTGCTGCTCTCTTATTTTAAATTTTGTGATT 3672
Db 2811 GAGGGCTGTGTTATGCTGCTTGTGAGTGCATATCTCTCTCTCTGCTGCTCATC 2870
Qy 3673 GTTGTCTATCAGAAACAAAGGGGTGTAATATCAGTTAAAGAAAGAAAGATGCC 3732
Db 2871 CTCTGCTTCAACAGCCAGCAAGGGGGCAATATCTCAATGAAGTAAAGAGACACC 2930
Qy 3733 CATGCTGACCTTGAATTCAGCTATGAGAAAGATGATGGGACATTTGGAAATACAT 3792
Db 2931 CAGGTGACCTGAGGCGCGACCGATGAAGATGAGACCTTCGCGAGTACAGTCCCTG 2990
Qy 3793 GATGCAAGAGACCAAGACCTTTGAAAAAGAAAGTGAATCTCTTCAACAGAGACTGTG 3852
Db 2991 GAGAGTGAACAACAGGAGAAAGGCTTTGGACAGCAGCATGCTCAACGGGGAATC 3050
Qy 3853 AAAAAAGATAGTGAACGACAGCTAGTGAATGAGAGAGGGGTAAATGAGCCAGTTC 3912
Db 3051 AAGCCCTGGGAGTGAACGACAGCTGGCGGATTAAGGGGAGCGGTGATTCAGTTC 3110
Qy 3913 AATGAGATGCTCTTATTTGACATATCAGTGTAAAGAAAGAGCCGGCTGAA 3972
Db 3111 AAGGAGATGCTCTTATTTGACATATCAGTGTAAAGAAAGAGAGGAGGCGGAGG 3170
Qy 3973 GGAACGAAGGCTCAGAGG 3991
Db 3171 GGCAATGACAGCTCAGGGG 3189

RESULT 10
US-08-427-497E-4
Sequence 4, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Inhibitor
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2600
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: 4
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human L1CAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 1108 to 3708
US-08-427-497E-4
Query Match 5.5%; Score 228.8; DB 2; Length 2600;

Best Local Similarity 45.9%; Pred. No. 3,4e-57;
Matches 1224; Conservative 0; Mismatches 1367; Indels 75; Gaps 10;

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OY 1306 GGAAGTCCCAATAGAAATTCGCCCCGTATGATACCCAGACAGAAATAATATATGCGCATACATT 1365
Db 1 GGGATTCCTGTGAGAGAGCTGGCCAAAGACACAGAAATACCGGATTCAGGGTGGCCGCTG 60
OY 1366 ATTTTTCATTAATGTTGAGAAAGATCAATGTCAGTATATCATGTCAGTACGCTCTATATGAA 1425
Db 61 ATCTGAGACAGCTGAGAGCCAGTACACATATGTATACCAATATGTAAGCCCGCAACCGG 120
OY 1426 TATGATATTACTGCAAAACGATTTGTAATGTGCTGAGTCCAGCCACCAAGATCTTC 1485
Db 121 CAGGGGCTCTTGCTGGCCAAATGCTACATCAATGTTGTCCAGCTGCAGACCAAGATCTG 180
OY 1486 AACACTGCAAAACACACTTACAGAGCTCATTTGCAAAAGAGCCGCTTTATATAGCTGTGC 1545
Db 181 ACTGCGGACATCAACGATACATGAGCTGTCAGAGGAGCACTGCCCTTCTGTGTCAG 240
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Db 241 GCTTCGAGAGCCGCTGTGCTCCAGTGTTCAGTGTGCTGAGAGATGGACACAGTGTCTT 300
OY 1606 CATGAAGATATTATATGTTTACATGAAATGAACTTTGAAATCAAGATGCTACATG 1665
Db 301 CAGGAGAAAGGCTTCTCCCTATATGCCAATGGGACCTGGGCACTGAGACCTCCAGGCC 360
OY 1666 ATGCTTAAAGAAATTCCTGTGGCCCAAAAGACATGACAGAACTTATACGTGTGTGA 1725
Db 361 AATGACACCGGACGCTACTTCTGCTGGCTGACCAATGACCAAAACATGTATACCATATG 420
OY 1726 AGGAATTAATTAAGGATGGAAGAAAGATGAAGTTCACTTACGCGGCAATATGAGTGTG 1785
Db 421 GCTAACCTGAAGTTAAAGATGCACTCAGATCATCAGAGGAGCCCGGACACATATGAG 480
OY 1786 CAAAGAGGAGCATGTGTCTTTGATGCAAAAGTGAACATGATCAACCTTATCCCTC 1845
Db 481 AAGAAAGTTTCAAGGTTGACCTTACGTCGACAGGCTCTCTTGAACCTCTTGCAGGCC 540
OY 1846 ACTGTCTGTGGTGAAGCAACAGGGAATGCCCCAGTA-----TGAAGGTTTC 1896
Db 541 AACATCACCCTGGTGGGACGGTCCAGACCTCCAGAGCTTGGGGACAGTGCATAGTAC 600
OY 1897 ACTGTGACAGAGGATCATAGTGTAGTGAATGTCAATGTCAGTACGATGACAGCGGACCTAC 1956
Db 601 TTCAATGAGAGATGGGCTGTGATCAACAGCTGGACTACAGCAACAGGCAACTAC 660
OY 1957 AGGTGTGGCCCAACCACTGTGACAGAGCTCTCCGCAAGCGCTGTGCTTACGCTTGT 2016
Db 661 AAGTGTGGCCCAAGTACGAGCTGTGATGTGTGAGAGATAGGCAAGCTCTTGTGTGTG 720
OY 2017 GCTCTACTTCAACTCCAGCTCCGTTTACATGATGTCCTCAATCTCTCTTGAATTGAA 2076
Db 721 GGGAGGCTT-GGGCCGGTCCACAGCGTGTGCTGTGACCTGCACTGCTGCGACGAG 779
OY 2077 CTGACGATCACTTGAACAAAGTGTTCAGCTGTCAATGACCCAGGCGATGACACAT 2136
Db 780 C-----CAGTGGCGGTCTCTGAGTCTTCAAGACCAACAT 819
OY 2137 ACCCCCTATACAAATTCATCATGATATGAAGATGCAATGCAACAAGCGGGCTGTGG 2196
Db 820 GCCCCCTATGAGAAATATGACATTTGATTTGAGACAAAGAAATGCGCTGAAATATG 879
OY 2197 CACCAACAACTGAAGTTTCTGAGACACAGACCAAGCCCAAGTGAAGTGTCTCTTAC 2256
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Db 1000 GTCTCTGAGACTGTGTGACACCTTGAGGAGCCCAAGAGAAACCTGTGTGATGTGAG 1059
OY 2377 GGAAGTGGATCAGAGCTGATTAATTTGAGATTATAGTGGAGCCCTGATGATGTTTGA 2436
Db 1060 GGGAAAGAAATGAGACACCAATATGTATCATCAGTGAAGCCGCTCGGTGATGAGAC 1119
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OY 2677 AATGTGTGAACATGACTTACCCAGGTGACCTGGGACCCAGTACTCTGAAAGATC 2736
Db 1357 GAAATCTCAACTCAAGTGCCTGTGCTCAAGTGGCGGCTGGGACCTGGCCCAAGTTC 1416
OY 2737 CAGAGACCTTCAAGGCTATGATTTATATGGAAGACCCAGATTCATCTTAAAGA 2796
Db 1417 AAGGCTCACTCCGGGATCAATGTGACGTGAGAGGAGGAGCACTGAGAGAACAC 1476
OY 2797 AACAGACTCATTTGAGAAAGATCTCTCACTTCAAGGAGCAAGACTCATGAGCAT 2856
Db 1477 AGCAAGAGACATTCACAAAGACATGTGTGTGTGCGGCCAACAACAGCTGTATC 1536
OY 2857 TTGCGGGGCTAGAGCCCTTTAGCACTACCTGCACTGAATGTCCAGTGTCAATGGGAA 2916
Db 1537 CTCACTGTGCTGCGGCTCTATGCTCTTACACCTGAGGTGCAAGGCTTTTAAACGGGCA 1596
OY 2917 GGGAGAGGCCCAAGCCCTGACAGAGTCTTATATCTCAGAGAGAGTCCCGCAGTGT 2976
Db 1597 GGAATGGGGCCCGCAGC---GAGTTACCTTACAGACCCCAAGAGAGTGTGTGCGCAC 1653
OY 2977 CCTGTCTTTGAAATGTGATTCACCACTGAGCTCTTCACTTGTGAAATGGATCCA 3036
Db 1654 CCGAGAGGCTTGAACCTGAGAGTGCATGGAACACCAAGCTGTCTGTGCTGCGCAGCCC 1713
OY 3037 CCGAGCCACCCGATGGAATTTTGAACAGATACACTTAAATATCAGCAATTAACAGC 3096
Db 1714 CCATCAGCAACAGCGGTGTCTACCGGCTACGTGTCTCTTACACCC-----C 1764
OY 3097 ACATGAAATTAAGCCCTCTGTATTTGAAATTTCTGCGCAACAAGACAGGTGACT 3156
Db 1765 CTGATGAGAGGGGGAAGGGGCACTGTCTTCACTTGGGACCCGAACTTGGGACA 1824
OY 3157 TTAATAAATTTAAATTTGACACTGATATAAGTTTATTTCTATGCAACAAATCAGCA 3216
Db 1825 CACAACTGACCGATCTCAGCCCACTGGGCTACCGCTTCACTTCACTTCACTTCACTTCA 1884
OY 3217 GGATCAGAAAGTCAATTAACAGAGAAACAGTACACTGTGTGATGAAGCTGTATTTCT 3276
Db 1885 AAAAGAGGCGCT-----GGTGAAGCATGTGTGAGGGAAGAGGACACTA 1927
OY 3277 CCACTGATGTATGTGTCAGGCAAGTTCAAGTGTAAATACAGATCAGCAATCTTACT 3336
Db 1928 TGGCTTGTCTGGGATCTCAGATTTTGGCAATCTCAGCCACAGCGGATGAAACTTCA 1987
OY 3337 GCTGAGCTGCTGAGACTTATGCAATATCAGTTGGAAATATGAGGAGCAGAGCATGTG 3396
Db 1988 GTGTGTCTCTGTGCTCCCAAGAGGGCCAGT--GCACTTCAGGTCTCATATTTGT 2045
OY 3397 AACTTTATTTGATATATGTGTATGACAGCAGCAAGAAAGATGGAAGAAATTTGA 3456
Db 2046 CAAAGCTTTGGGAGAAAGAGGAGGTGGGCTTCCCTTTCG-----CAACAGTATGTG 2097
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Y 3457 AATGGTCTCGAGGCTTCTTTGGTTAAAGGGCTTAAGCCAGCAAGCATACAAAGTT 3516
Db 2098 AGCTACAAACCAAGAGCTCTTACACGACGATGGACCTTGACCTGACCTACTACAGATC 2157
Y 3517 CGAGTTGGTGCCTGTGGGGGACTCTGGTTTTGTGAGTTCAAGAGATGTGTTTGAACAGGC 3576
Db 2158 CACTTGTTTAAGAGAGAGATGTTCCGGGACCAAAATGGCTGTGAAACCAATGGCACAGGC 2217
Y 3577 CCAGCGATGGCAAGCCGCGAGTGGATATTGCACTCAGAGGCTGGTTCA TTGGTCTGATG 3636
Db 2218 CGCGGAGAG--CTCCCTCTGCTGGCTTGCCACTGAGAGGGCTGGTTCA TCGGCTTTGTG 2274
Y 3637 TGTGCTGTGCTCTCTCTTAATCTTAATTTTGTGATTTGTGCTTCA TCAGAAAGAAAG 3696
Db 2275 AGTGCATCATCTCTCTGTCTCTGCTCTGCTCACTCTCTGCTTCA TCAAGGACAGAG 2334
Y 3697 GGTGTAAATATCCAGTTAAAGAAAGAAAGATGCCCATGCTGAC CCGTTGAAATCCAGCTT 3756
Db 2335 GCGCGCAATATCTCAGTGAAGGATTAAGAGAGACACCCAGGTG GACTCTGAGGCCGACCG 2394
Y 3757 ATGAAGAAGATGATGGGACATTTTGAAGATACAGTATGCAAG ATGCAAGAACCAAGCCTTTG 3816
Db 2395 ATGAAGAATGAACCTTGGCGAGTACAGTCTCTGGAAGTGA CAAACAGAGAGAAAGGCC 2454
Y 3817 AAAAAAGAAAGTGCAACTCTTTCAGACAGACCTGTGAA AAAAAAGAAATAGTACGACAGC 3876
Db 2455 TTGGCAGCAGCCAGCCATCGCTCAAGCGGAGATCAACCC CTTGGCAGTACACAGAC 2514
Y 3877 CTAGTTGACTATGAGAAAGGGTTAATGGCCAGTTCATATG AGAGATGCTCTTTATTTGA 3936
Db 2515 CTGGCCGATTATGGGGGCGAGCTGAGTGTTCAGTTCAACG AAGATGTTGTTCAATTGGC 2574
Y 3937 CATACAGTGCTAAGAAAGAGAAAG 3962
Db 2575 CAGTACAGTGCCAGAGAGAGAAAG 2600

RESULT 11
US-08-506-296B-3
Sequence 3, Application US/08506296B
Patent No. 6313265
GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: Crossin, Kathryn L.
TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBROBLAST TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: U.S.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 488.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 3:

```

```

? SEQUENCE CHARACTERISTICS:  

? LENGTH: 3991 base pairs  

? TYPE: nucleic acid  

? STRANDEDNESS: double  

? TOPOLOGY: linear  

? MOLECULE TYPE: cDNA  

? HYPOCHREITICAL: NO  

? ANTI-SENSE: NO  

? FEATURE:  

? NAME/KEY: CDS  

? LOCATION: 59...3859  

?  

US-08-506-296B-3
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Query Match	3.8%;	Score 157.4;	DB 4;	Length 3991;
Best Local Similarity	44.2%;	Pred. No. 7.3e-36;		
Matches 1106;	Conservative	0;	Mismatches 1266;	Indels 129; Gaps 6;

OY	233	AAGACTTGGTACAGCTCCAAACCAATCACCCCAACAGCTCTCCAAAGATTACATTATGGACC	292
Db	147	ACGATTTCTGCGAGGCCCGCCGAGGCTGACGGAGGAACCCCGGAAACAATCGGTGCTTCC	206
OY	293	CTCGGAGAAATTTGTAAATCCAGTGTGAAGCCAAAGGGAACCGGCCCAAGCTTTTCT	352
Db	207	CCAGTGATGATCGTCTCTCAAATGCGGGCCACCGGGAAACCCCGCTCCAGTACCGAT	266
OY	353	GGACCCCGTAATGGGACCTATTTTGCATCTGATTAAGAACCTCTGTGTACCAATGAAGCCTG	412
Db	267	GGAGCCGTGAGGATTCAGCCCTTTCGTCCCGGAGAGCACGGGGGGGTCTCGGTGTCCCG	326
OY	413	GCACAGAACGCTCATTAATTAACATCATGAGCGAAGGGGAAAGCTGAGACTTATGAAGAG	472
Db	327	GATCGGGGACTTTGGTATCAACGCCACGTTGGCCGGCCGAGCTCAG-----GGGC	377
OY	473	TCTATCACTGATACAGAAAGAACCGCGAGCTGCGATTTCTAATAACATTGTTTTC	532
Db	378	GCTTCGCTGTGTGCGCAACACGGGTTGGGACCGCGTGTCTCCGAGGCCAACGTCA	437
OY	533	GCCCATCCAGATTCACATTTGTGAGCAAGAAAGAAACTTGAAACAATCACATCTTCAAAGTG	592
Db	438	TCGCGGAGAAACATCCGACGTGCGCGAGAGGAAGTATACCCGGTGGAGGTGGAGGAG	497
OY	593	GTCAGTCTTTAGTACTTCCCTGCGAGACCCCCCAATTGATTACACACCATTAATATTTT	652
Db	498	GGGACCCCGTGGTGTGCTGCTGTGACCCCGGAGAGGCGTGTTCCTCTAAATCTAAT	557
OY	653	GGATGGAATATCTCTTTCAAAGACTTCCACAAGATGAGAGATTTCTCAAGGTTTGAATG	712
Db	558	GGCTCAACAGCGACATCGTTCAATCGCTTCAGAGAGAGGGGTCTCTATGGGGCAGAGATG	617
OY	713	GGGACCTTTATTTTTCATATGCTCTCCGAGAGCACCGCGAAGACTATATCTGTATG	772
Db	618	GGAACTTACTTCTCCAAACGCATGATGGGGGACAGCAACCCGAGCTACATCTGCGACG	677
OY	773	CTAAGTTTAATCACTACTCAAACCATACAGCAGAGCAACCTATTTCTGTGAAGGTGATT	832
Db	678	CTCACTTCTCGGCCCCCGCACCAATCATCAAGAAAGACCCCTCGACCTCCGCGTGGCCC	737
OY	833	CAGTGGATGAATTTGAATAGCACTAATAGTGTCTAATTTAGTGACACTGATTTTATGGTG	892
Db	738	CCAGTAATG-----	746
OY	893	CTAAATCAAGTAGAGAGAGGCCACCAACATTTTAACTCAGAAAGCAATGCAAGTAAACA	952
Db	747	-----CGGTTCCGATCCCGCGGCCCGCGCTGCTGTGCGCCCGGACCCCAAGACCA	800
OY	953	AAGAGAAATTTAAGAGAAATGTGCTTTCACTGGAATGCAATTTGCAAGAGATCTGCTACCC	1011
Db	801	CCATGCGCCCTCCGGGGGGGACAGCGTCTGTTGGAGTGAATGCTTAAGGGGCTCCCACTC	860
OY	1013	CAATTATTACTGGGCAAAAGGAAGTGAATGCTACCCAAAAGACGACAGTTTATPAGA	1071
Db	861	CATGGGTCCGATGCGCGGCGCTGAACGG-----CCCTCTCTCCCGGGCGCGTTGGAA	914

1073 ACTTGAGAAAACCTTGACAGATCATTGTTTCAGAGCAGACTCTGGAATTAACCAAT 1132
1133 GATTGACAAAATATGATTAAGAGCATTCCACATACCAATTTCTGTAAAGTTAAAGCCG 1192
975 GTGTGCTGAGAAACGGAGAGGAGGAGCCAGAGGAGCCAGACGCTGACGTTGAGAGCCG 1034
1193 CTCCTACTGATGATCAGAGCCCTTCAAAATCTTGTGCTGTCCAGAGAGGATGAGGACT 1252
1035 CCCCATATTGGGTGCGGCGGCGCCACAGAGTGGGTCTTGCGGCGGAGGAGAGCGGAGGC 1094
1253 TGATCTGACAGCTAATGGAACCCCAACCCAGAAATTAGCTGTTTACAAATGAGAGTC 1312
1095 TGAGCTGCGAGGTGGGGGGGAAACCCCAATTCATATGAGCATCAATGGGGTTC 1154
1313 CAATAGAAATTTGCCCCCTGATGACCCCAAGAGAAATTAATGCGCATACATTAATTTT 1372
1155 CCATGAGAGCTGCGGGGGGAGC--GGCGGTGCTGCGGGGCGGCTTTGTGCTTTC 1211
1373 CAATGTTCAAGAAAGATCAAGTGCATATATCAAGTCAATGCTCTAATGAATATGAT 1432
1212 CGAGCTGCGGCGGCGGAGCAGACGCGGCTCTGATGCGAGGAGAGAAACCGCACGCGC 1271
1433 ATTTACTGGAACACGCAATTTGTAATGTGCTGAGCCACCAAGATCTTACACACTG 1492
1272 CCTATTGCGCAACGCTTCTGCAAGTGTGAGAGCTGCGCTCGAATGCTGAGAGCGCG 1331
1493 CAAACACACTTACCAAGGCTATTTGCAACAGGCTGCTTACTAGACTGTGCTTTT 1552
1332 ATGACACAGGCTACGAAAGTGTGGAACCAACAGTGTCTTCTGCACTCAGAACCTTG 1391
1553 GGTCTCTCCCAACCATGAGTGTGTTAAAGAGCTAAGAGAGTCTTTCATGAG 1612
1392 GGGCGCGCGCGCAACGTCGAGTGTGCTAAGCCCACTTTGAGCGGCTCTGACAGAGC 1451
1613 ATATTATGTTTATCATGAAATGGAATCTTGAATCAAGATGCTACATGATGCTTA 1672
1452 ACCGATCCTTGTTTACCAATGAGAGCTTGTGAGTGTGCGGGGGGGGAGC 1511
1673 AAGAAATTCCTGTGCGCCAAAGAGACATGACAGAACTTATAGTGTGTTGCAAGATA 1732
1512 GGGGGGTCTACACTGATGAGCCCAAAAGCCACAGCAAGCAGACCTCAAGCGCTCC 1571
1733 AATTAGGATGCGCAAGATGAGTGTCACTTACAGCCCAATATGAGTGTGCAAGAG 1792
1572 TGGAGGTGAGACCCCGCCGAAATTTGCGCCCGCGGAGCGCACCGCCCAAAAG 1631
1793 GAGCATGAGTGTCTTTGATGCAAAAGTGAACATGATGACACTTATCCCTCAGCTGCC 1852
1632 GGGAGACGATGACCTTTCACTGCGGGGCGACCTTTGACCCCGCGTGAACCCCGGGAGC 1691
1853 TGTGCTGAGAGCAACAGGAACTGCGCAGTGAATGAAGTTCACTGTTGCAAGATC 1912
1692 TGGCATGCTGCGGGGGGGGAGCGCTCCGAGACACCCCGGTATGCGTGGCGGCG 1751
1913 ATCTAGTGTACATGATGATGATGAGATGAGACGCGGACCTTACAGTGTGCGCAAA 1972
1752 AATATGAGTGTCAACGTGATCTATGAGGAGAGGAGGACATTCAGTGTGCGGCTTCA 1811
1973 CCACTCTGAGACAGCTCTCCGACAGGCTGTGCTTACGCTTGTGCTCTACTCCAACTC 2032
1812 CCCCTCTGACTCCGCGAGGCGGAGCGCAAGTGTGAGTGTGCGGCGCGCCCA---- 1867
2033 CAGCTCCGTTTACGATGTCCAAATCTCTCTTTGACTTGAATGACATGACATCACTTG 2092
1868 -----TCCGCGACTTCAAGGATGAGTGGAGC 1898
2093 ACAAAGTGTGAGTGTGATGAGACCCGAGGAGTGAACAATAGCCCATTAACAAT 2152
1899 AACACCGGTGCGCTCAGCTGACCTCCGAGGAGAGCAATCAACGCCCCCATAGAAAT 1958
2153 TCATCATGAAATATGAAATGATGACAAAGCAGGCTGTGGACACCAAACTGAAG 2212

1959 TCGTGTGAGAGAGAGAGAGAGAGAGATCTTCAAGCGGGTTTCGAGCGGCTGAGC 2018
2213 TTTTGGAAACACAGACCAAGCCAGCTGAGCTGTCTCTTACGTTGAATCACTACTCTCC 2272
2019 TTCCGGGAGCGGTGAGACGCCCCCTTCGCTGTCTTCCCATAGGAGGTTCCGCTTCC 2078
2273 GCGTATGAGCAGTGAACAGCATTTGGGAAGAGCTTCCAGAGGAGGCTGTGAGCATATT 2332
2079 GGTGTGTGCGCTTAAACGCTACAGAGAGGAGGAGACCAAGCCCCAGCGCCCCCATATG 2138
2333 TGACGAAAGCTCAGAACCAATTAATAACCCCAAGCTGTGAGAGACTGGGATGAGC 2392
2139 AGACCCCCCGCGCTCCGAGCGCAACCCGAGGAGGAGTCCATGAGGAGGCAATGAGA 2198
2393 CTGATATTTGGAGTTTACGTGAGAGCCCTTGAATGTTTGAATTAATGAGGCGAGCC 2452
2199 CCGGACCTGCTATCACTGTGAGAGCCCTTCCCGAGGCTGTGAACGCCCCCTGAG 2258
2453 TTCAATGAAAGTTAGTGTGCGCGCCAGAAAGATGATGATGATGATGATGATGATGATG 2512
2259 CCGGCTACCGCTGTGAGTGTGCGGCGCATTTGAGAGACCCGCGGGGGGCGCTTGGGGG 2318
2513 TGGCAATGTATCAATATATTTGTCTGAGGAGCGCAACCTTTGTT----- 2559
2560 -----CAATCTGATCAAAAGTTCAAGGCTCTGAAATGACATGAGGAGTTTCCCGCGAGC 2611
2379 GCTTACGCTCTTCAATGCGCGCTGACGCGCTGTAACGAGCGGAGAGGACCGGAG 2438
2612 CAGCTGTAGTATGAGGAGATTTCTGGAAGAGACTCCCATGAGTGTGCTCTGGAAGTGC 2671
2439 CGACCCCGCGGTGGGGGAGACGCGGAGAGACTGCTGTTGTTTACCTTGAATGTGG 2498
2672 GTGTGATGTGTGTAACAGTACTTGAAGGAGTGCCTG 2712
2499 GGTGGAAGTGTGTAACAGAGACCGTGTGAGTGTG 2539

RESULT 12
US-08-427-497E-5
; Sequence 5, Application US/08427497E
; Patent No. 5969124
; GENERAL INFORMATION:
; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
; Patent No. 5969124
; TITLE OF INVENTION: the Nucleotide Sequence
; Characterized thereby
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fay, Sharpe, Beall, Fagan,
; ADDRESSER: Minnich & McKee
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
; MEDIUM TYPE: storable
; COMPUTER: Compaq Prolinea 5100e
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,497E
; FILING DATE: April 24, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/904,991

```

      1 FILING DATE: June 26, 1992
      2 ATTORNEY/AGENT INFORMATION:
      3 NAME: Minnich, Richard J.
      4 REGISTRATION NUMBER: 24,175
      5 REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
      6 TELECOMMUNICATION INFORMATION:
      7 TELEPHONE: (216) 861-5582
      8 TELEFAX: (216) 241-1666
      9 TELEX: (216) 980162
     10 INFORMATION FOR SEQ ID NO: 5:
     11 SEQUENCE CHARACTERISTICS:
     12 LENGTH: 1794
     13 TYPE: nucleic acid
     14 STRANDEDNESS: single
     15 TOPOLOGY: linear
     16 MOLECULE TYPE: nucleic acids
     17 HYPOTHETICAL: irrelevant
     18 ANTI-SENSE: no
     19 ORIGINAL SOURCE:
     20 ORGANISM: homo sapiens
     21 INDIVIDUAL ISOLATE: 17-18 week fetus
     22 IMMEDIATE SOURCE:
     23 LIBRARY: Stratagene cDNA Library 936206
     24 CLONE: 17
     25 PUBLICATION INFORMATION:
     26 AUTHORS: Hlavin, Mary Louise
     27 AUTHORS: Lemmon, Vance
     28 TITLE: Molecular structure and functional testing of
     29 TITLE: human L1CAM: an interspecies comparison.
     30 JOURNAL: GENOMICS
     31 VOLUME: 11
     32 ISSUE:
     33 PAGES: 416-423
     34 DATE: 1991
     35 RELEVANT RESIDUES IN SEQ ID NO: 2731 to 4503
     36 US-08-427-497E-5
     37
     38 Query Match 3.6%; Score 148.4; DB 2; Length 1794;
     39 Best Local Similarity 60.3%; Pred. No. 2,1e-33;
     40 Matches 245; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
     41
     42 Db 3605 TTGCAACTCAGGGGCTGTTTCATTTGTCATGATGTCGTCGTTGCTCCTTATCTTAAATTT 3664
     43 641 TCGCCACTGAGGGCTGTTTCATCGGCTTTGAGAGCCATCATCTCCTGCTCGTCC 700
     44
     45 Db 3665 TCGTGATTGTTGCTTCATCAGAAAGAAAGAGGCTGTAATATTCAGTTAAAGAAAGG 3724
     46 701 TGCTCATCCTCGCTTCATCAAGCCAGCAAGGCGGCAAAATACAGTGAAGGATAAGG 760
     47
     48 Db 3725 AAGATGCCCATGCTACCTCGTAATCCAGCTTATGAAGAAAGATGATGGACATTTGGAG 3784
     49 761 AGGACACCCAGGTGACTCTGAGGCCGACCGATAAAGATGAGACCTTGCGGAGTACA 820
     50
     51 Db 3785 AATACAGTATGCAGAAAGCCACAAGCCTTTGAAAAAAGAAAGTGAAGTCACTCCTTCAGACA 3844
     52 821 GGTCTCTGAGAGTACACAGGAGAAAGGCTTTGGCAGACGACCGCATTCGCTCAACG 880
     53
     54 Db 3845 GGAAGTGTGAAAAAAGAAAGATAGTACGACAGCCTAGTTGACTATGAGAAAGGGTTAAAG 3904
     55 881 GGGACATCAAGCCCTGGGCGAGTACGACAGCTGGCCGAGTTATAGGGGCGACGTTGATG 940
     56
     57 Db 3905 GCCAGTTCAATGAGATGGCTCTTTATTTGGACAATACAGTGTATGAAGAAAGAAAGAGC 3964
     58 941 TTCAATTCACAGAGATGTTGTTTCATTTGGCCAGATACAGTGGCAAGAAAGAGAGAGG 1000
     59
     60 Db 3965 CGGCTGAAGAAAGAAAGAAAGCTAGAGGCACTTCTCGTCAACGC 4010
     61 1001 CGGCAAGGGGCAATGACAGCTCAGGGGCCACTTCCCAATCAACCC 1046
  
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3173
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 128..322
US-09-621-976-3173

Query Match          3.1% Score 128.2; DB 4; Length 455;
Best Local Similarity 91.3%; Pred. No. 8.7e-28;
Matches 136; Conservative 0; Mismatches 13; Indels 0; Gaps 0.

OY      2944  GTCTTAATATCTCCGAGAGAGTCCCGAGTCCCTCGTCTTTGAAGATTGTGAATCCA 3003
DB      240  GACTGTAAGTTCTACACGTGAAGTCCCGAGTCTCCCTCGTCTTTGAAGATTGTGAATCCA 181

OY      3004  ACACTGACACTCTCTCACTTTGGAAATGGAGATCCACGAGCCACCCGGAATGGCATTTTGACA 3063
DB      180  ACACTGACACTCTCTCACTTTGGAAATGGAGATCCACGAGCCACCCGGAATGGCATTTTGACA 121

OY      3064  GAGTACACCTTAAGATATACGCCAATTA 3092
DB      120  GAGTACACCTTAAGATATACGCCAAGTA 92

RESULT 14
US-08-427-497E-6
Sequence 6, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427.497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.

```

REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CMR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 960162
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: C2
PUBLICATION INFORMATION:
AUTHORS: Hlaavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human L1CAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: -26 to 1016
US-08-427-497E-6

Query Match 2.4%; Score 99.8; DB 2; Length 1042;
Best Local Similarity 48.8%; Pred. No. 4e-19;
Matches 303; Conservative 0; Mismatches 312; Indels 6; Gaps 1;

239 TGTGACGCTCCAAACCATCACCACAGCTTCCTCCAAAGATTATGACCTCCGGG 298
118 TGAATGAGCACCCTGTCATCAGGAACAGCTTCACGGGCTGTGTCCTCCACAG 177
299 ACAATATGTAATCCAGTGTGAAGCAAGGAAACCCGCCCAAGCTTTCTGGAACCC 358
178 ATGACATCAGCCTCAAGTGTGAGGCGAAGGCCCAAGTGCAGTTCCGCTGACCA 237
359 GTAATGGAAGTCAATTTGACATCGATTAAGACCCCTGTGTGTCAGCATGAA-----GCCGTG 412
238 GGGATGTGTCACTTCAAAACCAAGGAAGAGCTGGGTGACCGTGTACAGTGCAGCC 297
413 GCAAGGAACGCTCAATTAATTAATATGAGCAAGGAAGTGAAGCTATGAGAGG 472
298 ACTGTGGCTCTTACATCAGGAGCAAGCAAGCACTTTGTCTGAGAGTTCCAGGGCA 357
473 TCTATCAGTGTACAGCAAGGAAGCAAGCGGAGCTCAGTTTCTAATAATGTTGTC 532
358 TCTACCGCTGCTTGTGCAAGCAATAGCTGGGCAACCGCATGTCTCCATGATCCGCTCA 417
533 GCCCATCAGATCAGCATTTGTGAGCAAAAGAAATTTGAACCAATCACTTCAAGT 592
418 TGGCCGAGGGTGCCCCAAGTGAGCAAGAGCACTGAAAGCCGTGAGGTGAGAGAG 477
593 GTACGCTTTAGTACTTCCCTGAGAGCCGCCAATTGATTAACCACTATATATTTT 652
478 GGAAGTCAATGTGTGCTTGAACCTTCCGCCAAGTCAAGAGCTTCCGATCTACT 537
653 GGATGATATATCTTTCAAGACTTCCCAAGTGAAGAGTTTCTCAAGGTTTGAATG 712
538 GATGAAACAGCAAGATCTTGCAATCAAGCAGAGAGAGGGGTGAGTGGGCGAGAG 597
713 GGAACCTTATTTTTCATATGTCCTTCCAGAGAGACCCGCGAAGACTATATCTGTTATG 772
598 GCAACCTTACTTGTGCAATGTGTCACTCCGAGCAACCACTCAGACTATCTGCGACG 657

773 CTAGATTATATCACTCAACCATACAGAGCAACCTATTCTGTGAAGTATTT 832
658 CCCACTTCCAGAGCAGCAGACCATTCATCAGAAAGAACCTATCACTCCGGGTCAAG 717
833 CAGTGATGAATGAATGACA 853
718 CCACCAACAGCATGATTGACA 738

RESULT 15

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA

COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: PTZgpt-Fls

US-08-232-463-14

Query Match 1.6%; Score 65.2; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred. No. 2.6e-08;
Matches 13; Conservative 199; Mismatches 112; Indels 0; Gaps 0;

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1365 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1306
3745 GAATCCAGCCTATGAAGAGATGATGAGCAATTTGAGAAATCAGATGAGCAAGAC 3804
1305 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1246
3805 CACAAGCCTTTGAAGAAAGAGTGAAGTCTCTTCAAGCAGAGACTGTGAAAAAGAGAT 3864

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2004, 02:51:56 ; Search time 1625 Seconds
(without alignments)
11561.787 Million cell updates/sec

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Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	472.8	11.4	7491	13	US-10-435-751-151
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6	469.6	11.4	7570	13	US-10-435-751-18
7	469.6	11.4	7570	13	US-10-435-751-193
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9	469.6	11.4	7650	13	US-10-435-751-2
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11	469.6	11.4	7650	13	US-10-435-751-158
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14	469.6	11.4	7650	13	US-10-435-751-176

15	469.6	11.4	7650	13	US-10-435-751-182	Sequence 182, App
16	469.6	11.4	7650	13	US-10-435-751-188	Sequence 188, App
17	469.6	11.4	7650	13	US-10-435-751-194	Sequence 194, App
18	469.6	11.4	7651	13	US-10-435-751-207	Sequence 207, App
19	445.4	10.8	2462	16	US-10-104-047-78	Sequence 78, App
20	423.6	10.2	7686	13	US-10-435-751-14	Sequence 14, App
21	423.6	10.2	7686	13	US-10-435-751-181	Sequence 181, App
22	423.6	10.2	7686	13	US-10-435-751-183	Sequence 183, App
23	411.6	10.0	7602	13	US-10-435-751-10	Sequence 10, App
24	411.6	10.0	7602	13	US-10-435-751-169	Sequence 169, App
25	411.6	10.0	7602	13	US-10-435-751-171	Sequence 171, App
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27	404.4	9.8	7527	13	US-10-435-751-175	Sequence 175, App
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29	358.4	8.7	7563	13	US-10-435-751-16	Sequence 16, App
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31	358.4	8.7	7563	13	US-10-435-751-189	Sequence 189, App
32	357	8.6	6487	13	US-10-435-751-6	Sequence 6, App
33	357	8.6	6487	13	US-10-435-751-157	Sequence 157, App
34	357	8.6	6487	13	US-10-435-751-159	Sequence 159, App
35	351	8.5	4523	16	US-10-411-010-7	Sequence 7, App
36	351	8.5	4523	16	US-10-411-010-7	Sequence 7, App
37	348.4	8.4	7329	13	US-10-435-751-8	Sequence 8, App
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41	340	8.2	445	9	US-09-864-761-10809	Sequence 10809, A
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ALIGNMENTS

RESULT 1
US-09-919-039-279/c
; Sequence 279, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 279
; LENGTH: 6384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 201395.4C
US-09-919-039-279

Query Match 78.2%; Score 3233.6; DB 10; Length 6384;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;

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QY 61 TTGTAAGAGAGAAAGAAATTCAGTGTGAGTCTCAGACAGAGATTAGCTATATGAG 120
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DB	4215	GAAATATGAGTGTGCAAAAGAGGAGCATGTGTCTTTGAAATGCAAGTGAATCATGAT	4156
QY	1831	CACACCTTATATCCCTCATCTGTCTGTGGCTGAAGACAAACAGGAACTGCCAGATGAAG	1890
DB	4155	CACACCTTATATCCCTCATCTGTCTGTGGCTGAAGACAAACAGGAACTGCCAGATGAAG	4096
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1727 GGAATTAATTAAGGATGCAAGAAATGAAGTTT- ACTTACAGCCCAATATGCAATTG 1785
1600 GTCCGCTGAGGATTAAGAACCCCAACAGATCTACCGGATGCGGAGACAGGTGGC 1659
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1846 ACTGCTGTGGCTGAAGCAACAGGAACTGCCAGATGTAAGATTTCACTGTTGAC 1905
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1966 GCGAACACCACTGAGACAGCGCTCCGAGCGTGTGCTTATGCTTGTCTTACT 2025
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2326 CAGTATTTTACGAAGCTTCAAGACCAATTAATAACCCCAAGCTGTGAGAGATGGA 2385
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Db 2467 GGTATCTCCGAGAAATTAATCCAGGGGTGCGCCACTGAATGAATGATCCAGTCA 2526
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RESULT 3
US-10-435-751-4
; Sequence 4, Application US/10435751
; Publication No. US20040053348A1
; GENERAL INFORMATION:
; APPLICANT: Agnays, Inc.
; APPLICANT: Paris, Mary
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; FILE REFERENCE: 51158-20084.00
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 4
; LENGTH: 7491
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (272)...(3787)
US-10-435-751-4

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Query Match 11.4%; Score 472.8; DB 13; Length 7491;
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Matches 1467; Conservative 0; Mismatches 1507; Indels 30; Gaps 6;

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367 ACAGGTCCAAACCATCAATAAAGTCCAAAAGTTCCTTCCTTCGATGAGTA 426
303 TATGTATCCAGTGGAGGCAAGGAAACGGCCCAAGCTTTCTCGAGCCGTTAA 362
427 TTTTCAATTAAGTGAAGCTAAAGAAATTCAGAACCAACTTTTCGGAAGTA 486
363 TGGAGTCAATTTGACATGATTAAGACCTCTGTCACCATGAAAGCTGACAGAAAC 422
487 TGGCAACCTTTTATTTTCACTGACCATGGATTAATTCATGAAACATTCAGGA----- 541
423 GCTCATTAATTAACATCATAGAGGAGGAAAGCTGAGACCTATGAAGAGTCTATACATG 482
542 ----ACATTCAGAGTCCAAACGAGGGGACATATCTCATCTTCAAGGAAATACCGCTG 597
483 TACAGAGGAAGAAAGGAGAGTGCAGTTTCTAATTAACATTTGTCGGCCATCCAG 542
598 CTTTGCTTCAATAAATCTGGAAATCGTATGTAGAAAGAAATTAATTAAGTCCAAAG 657
543 ATCAACCATTTGGAGCCAAAGAAAACCTTGACCAATCACTTCAAGTGTCAAGCTTT 602
658 TGTTCCAAATTTCCCAAAAGAAAATTAATGACCTCTTGAAGTGAAGAGGAGATCCAT 717
603 AGTACTCTCCCTGAGACCCCAATTTGATTAACCAACCTTAATAATTTTGAATGATA 662
718 TGTCTCCATGCAATCTCCCAAGGCTCCACCTTTTACATTTATGTAGTAATAT 777
663 TTCTTTCAAAAGCTTCCAAAGTGAAGATTTCTCAAGTTTGAATGGGAACTTTA 722
778 TGAATTAAGAACATGAGAACAGATGAAGATGATCATGAGCAAAAGGAGATCTATA 837
723 TTTTTCCAATGTCTCCAGAGAGACCCGCAAGACTATATCTGTTATGCTAGTTTAA 782
838 CTTTCGAAAGTGAAGAAAAGAGACAGTGCATGACTGTGCTTTGCTGCATTTTC 897
783 TCATCTCAAAACCATACAGAGAGCAACCTATTTCTGTAGAGTATTTCACTGATGA 842
898 AAGATTAAAGACTATTTGACAGAAAATGCCAATGAATTAACAGTTTAAAGAA 957
843 ATTGAATGACATTAAGCTGCTAATTTGAGTGAACCTGATTTATGTGTCTAAATCAG 902
958 TGTAAATGACTCAAGTTTCAACAGAAATTTGTTCCAAAGGCAATTCATCAAGCAAG 1017
903 TAGAGAGAGGCCCAACATTTTAACTCCAGAAAGCAATGCAAGTAAACAAAGAGAA 962
1018 AAAAACCAAACTGTGTGCTCCACTGAGAGTGGCAAGTACTTCAATTAACATCT 1077
963 AAGAGAAATGTGCTTCACTGAGTGCATTTGCAAGAAAGACTGCTCAATTTATTTA 1022
1078 CAAAGGGGAAATCTGTCTGTGAGTGTGTTGCTGAAGGCTTGCCTCAACAGGTGA 1137
1023 CTGGGCAAGAGATGGAATGCTAACCCAAAACAGAGACGTTTATTAAGAACTTTGAGA 1082
1138 TTGGAACAAAATTTGGTGTGATCTTACCAAGGAGAGGAGCAAAAGAAAATTAATGCA 1197
1083 AACCTTGACATTCATTTCTCAGAGAGACCTGCAAAATTAACAAATGTTATACAA 1142
1198 GACTTTGAAAGATGAAGATTTCTCTACAGAGCAAAAGAAATTAATGCTGCACAGCAG 1257
1143 AAATGATTAAGAGCCATCAACCATATCTTTCTGTTAAGTTAAAGCGGCTCATATCTG 1202
1258 CAATTTCTTGGAAACAGCCACTACGATTTTCAAGTTATGTAAGAGAGCTCTCGCTG 1317
1203 GATCAAGCCCTTCAAAATCTTGTGTGTCTCCAGAGAGAGATGGACCTTATCTGCAAG 1262
1318 GACAAAGAAAGCTCAGAGTGTGTATATGACACCGAAGCAATGAGATCTTGTATGTGA 1377

1263 AGCTAATGCAACCCCAAAACCCAGAAATTAAGTGTGTTAAACAATGAGATCCCAATAGAA 1322
1378 GGCTAAGAGAGAACTCAACCAACATCAAGTGAAGATCAATGCTCCCAAGTGAACA 1437
1323 TGCCTTGAATGACCCACAGAAAAATGATGCGCATACATTAATTTTGAATGTTCA 1382
1438 TCATCTCAATTTG---CTGTGATGTTGTTTCCCAAGGAAATCACTTTTACCACTTCA 1494
1383 AGAAAGATCAAGTGCATATATCAATGCAATGCTCTAATGAAATTAATGATAATTTA 1442
1495 ACCAATATATCTGCTGTGTACAGTGTGAAGCTCAATGTCCATGGAATCATCTTTC 1554
1443 AAAGCAATTTGTAATGTGCTGCTGAGCCACCAAGATCTCTACACTGCAACACACT 1502
1555 CAATGCCAATATGATGTTGTGTGATGTCGTCATATGATTAACAACCAAGATGAGAA 1614
1503 CTACAGATCAATGGAACAGGCGCTTTACTAGCTGTGCTTCTTGGGTCTCTCT 1562
1615 TTAGGCTACAGTGTGGGTACAGTCTTTCTTACATTTGCAATTTCTTTCCTTCACTGA 1674
1563 CCCAACCATCGAGTGTGTTAAAGAGCTAAAGAAAGTCTCTTCAATGAAATATTAATG 1622
1675 GGCAATCTGTCTGTGCAAGAGTGAAGAGTGAACCCCTGAGGAGCAAGCGGTATCA 1734
1623 TTTACATGAAATGGAACCTTTGGAATCAAGAGTCTACATGATGTTTAAAGAAATTC 1682
1735 TATCTATGAAATATGCAATTTGCAATGCAACCAAGCAAGAAAGATGCTGGCTTTA 1794
1683 TGTGCCCCAAAGAGACATGACAGAACTTATACGTGTGTTGCAAGAAATTAATGAGAT 1742
1795 CTATGTTGGTGAAGAAATGCTATGAGAAATCTGCAATCAAGCAATTTGATATTAAG 1854
1743 GGCAAGATGAAAGTTCATTTACAGCCCAATATGCAATTTGCAAAAGAGAGATGAT 1802
1855 AAATGCTCAAAACCTTAAGATTTCTCTTAAGATCTGTATGCCAATTTGCAATGCT 1914
1803 GTCTTTGAATGCAAGTGAACATGATCAACCTTATCTCTGCTGTGCTGATA 1862
1915 TGAATTAATCTGTGAAGAAATGTGACTCATTTTGAACACAGTTTGAAGTTGCTCTG 1974
1863 GGAACAAGAGAACTGCCAGTATGAAGAGTTCATGTCATGAGATCATCTAGTGT 1922
1975 GAGTAAAGATGAGAAAGCTTTGA-----AATTAATGCAAGAGATGAGAGAT 2025
1923 AGCTATGTCAGTGAAGATGACAGGAGGACCTACAGTGTGTGCAACACCACTCTGGA 1982
2026 AATTAATGATGAGCTAATTTGACATATCTTAATTAATTTAGAGACCAAGATTTTA 2085
1983 CAGGCTCTCCGCAAGCTGTGTGAGTGTGCTCTTACTCAACTCCAGCTCCGT 2042
2086 CTGCTGTTCAGCTCATTAAGCTCTGACAGAGTCTCCGATA---TAACTCAAGTAACTGT 2142
2043 TTAAGATGTCCAAAATCTCTCTTTGACTTGAATCACTGACAGTCAACTTGAACAAAGT 2102
2143 TCTTAATGTTCCGATCCACAGAAACCTTCACTGTGTGAAGACGAACAGAGTGT 2202
2103 TCAGCTGTATGAGACCCAGGCGATGACAAACAATAGCCCCATTAACAAATTCATATG 2162
2203 TGGGCTGACCTGGAAGCTGAGCTGACCAACAGCAATATTTAGCGATATATTTGTA 2262
2163 AATAGAGATGCAATGACCAAGCCAGGCTGTGSCACACCAACTGAAGTTTCTGGAAC 2222
2263 AATTAAGAGAAACAAAGAAAGCTGGAAGGTGGAGAACTGACCAAGATCCAAAGAAA 2322
2223 AAGACACAGAGCCAGCTGAAGCTGTCTTACGTGAATCTCTCTTCCGCTGATAGG 2282
2323 GAAAACCAAGTATCTTAACTTTGCTTCATTTGTGAGATACAGTTTCAGGCTATAGC 2382
2283 AGTGAACAGATTTGGAGAGCTTCCAGAGAGGCTCTGAGAGATATTTGACAAAGC 2342
2383 CBTGAACAGATGAGAGAGATGACCTAGCCGCTGACAGCACTATGAAACACAGC 2442
2343 CTCAAGAACGATTAACCAACCCACAGCTGTGGAAGAGCTGGGATCAGAGCTGATTAAT 2402

Db	2443	AGCAGCTCCAGATAGGAATCCACAAAACATAAAGGTTAAAGCTTCAACCCAGGAAT	2502
Oy	2403	GGAGATTA CGTGAAGCCCTTGAATGTTTCGATCTAATGGGCCAGGCCCTTCACTACAA	2462
Db	2503	GATTATTAAGTGGAGCCCTTGAATTCATGGAGCAGATGGACCAAGGCTTAGAGTACAG	2562
Oy	2443	AGTTAGCTGGCCGCCAGAAAAGATGGTGAATGAATGACATCTGTGGTTTGGCAAATGT	2522
Db	2553	AGTGAACCTGGAAAGCCACAGGAGGCCCAGTGGAGTGGGAAGMAACAGTCAACAAAAC -	2622
Oy	2523	ATCCAAATATATTTGTCCTAGGCAAGCCCACTTTTTCATATCTGATCAAAAGTTCAAGC	2582
Db	2622	--ACACATTTGGGGTGAATGAAGCCCTGTCTGTCTATCCCTTTATGATGTCCAAAGTCCAGC	2679
Oy	2583	CCYGAATGACATGGGGTTTGGCCCCCGAGCCAGCTGTAGTCAATGGGACATTCGAGAAAGA	2642
Db	2680	TATCAATCAACTAAGATCTGGGCTGACCCCTCAGTCAATGACTCTCTATTTCTGGAGAA	2739
Oy	2643	CCTCCCAATGGTGCTCCTGGGAACGTGGTGTGAATGTGGTAAACGTAACCTTAGCCGA	2702
Db	2740	CTATCTGTATACAGCTCCAGTATCCATGGGGTGGACCTTATTAACATACATTAAGTTAA	2759
Oy	2703	GGTGACCTGGGACCAGTACCTCTGAAAAGCATCCGAGGACACCTAACAGGCTATCCGAT	2766
Db	2800	AGTATACCTGGTCAACAGTTCCAAAAGACAGTATATGACCTCTGAAAAGCTATACAT	2855
Oy	2763	TTACTATTTGGAAGACCAGAGTCTCTTAAAGAAACAGAGTCACTTGAAGAAAAGAT	2822
Db	2860	AAATTTGGTGAAGAAACAAAAGTCTGTGGATGGAGAAACATCCCAAGAAAGTGAAT	2919
Oy	2823	CCTCACTTTCCAGGCAAGACATCATGGCATGTTGCCGGGGCTAGAGCCCTTTAGCCA	2882
Db	2920	TCTAAGATTTTCAAGGACAAAGAACTCTGGAATGGTCTTCTTAGATGCTTTAGTGA	2979
Oy	2883	CTACACACTGAATGTCCGAGTGTCAATGGGAAAGGGGACCGAGCCAGCCCTGCACAG	2942
Db	2980	ATTTCATTTACAGTCTTAGCCCTATTACTCTTAAAGAGCTGGTCTGAAAGTGAACCTTA	3039
Oy	2943	AGTCTTTATATCTCCAGAAAGAGTCCCAAGTGTCCCTGTCTTTGAAGATTGTGAATCC	3002
Db	3040	TATATTTCAAACACAGAAAGAGTACCTGMAACGCCAATTTTCTTAAAGTCACTCAAGT	3059
Oy	3003	AACACTGGACTCTCTCACTTTTGGAAATGGGATCCACGAGCCACCCGAATGGCATTTTGA	3062
Db	3100	TGATTAAGACACTGGCACTTTATCTTGGGGCACTACCTAAGAAATTAAATGAAACTTAAC	3159
Oy	3063	AGAGTACACTTAAAGTATCAGCCATTTAACGACACATGAATTAAGCCCTGTGTGA	3122
Db	3160	TGGCTATCTTTTGCATATCAGATTAATAAAGACACTACGAGATTTGAGAAATTAAATGA	3219
Oy	3123	TTTGAATAAT---CCTGCCAACAGACACGGTGACTTTAAAAAATTAAATTTCAAGAC	3179
Db	3220	TATTAACCTTACAACTCATCAAGGCCAGCTGGGCACTCTCAAACTGAAATGCACTAC	3279
Oy	3180	TCGATATATAGTTTATTTCTATGCAAAACATCAGCAGATCAGGAAGTCAAAATTACAGA	3239
Db	3280	CAAGTACAAATTTACTGAGGGCTTGCACTTCAAGGGCTGTGGAAAAACGATACGGA	3339
Oy	3240	GGAA 3243	
Db	3340	GGAA 3343	

APPLICANT: Baitano, Arthur B.
 TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 TITLE OF INVENTION: Entitled 282p1g3 Useful in Treatment and Detection of Cancer
 FILE REFERENCE: 51158-20084.00
 CURRENT APPLICATION NUMBER: US/10/435,751
 PRIOR FILING DATE: 2003-05-09
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 NUMBER OF SEQ ID NOS: 208
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 151
 LENGTH: 7491
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-435-751-151

Query Match 11.4%; Score 472.8; DB 13; Length 7491;
 Best Local Similarity 48.8%; Pred. No. 1,1e-128;
 Matches 1467; Conservative 0; Mismatches 1507; Indels 30; Gaps 6;

QY	243	ACAGCCCTCCACCATATCCCAACAGCTCCCAAAAGTTATCATTTATGACCCCTCGGAGAA	302
DB	367	ACAGCTTCCACACATCATTAACACATCAAAAGTCCAAAGTTCCTTCCCTTCGATGAGTA	426
QY	303	TATGTATTCACAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTCGAACCCGTAA	362
DB	427	TTTTCAAATTGAAATGTGAAGCTAAAGAAATCCAGAACCAATTTTGTGTGACATAAGGA	486
QY	363	TGGAGCTCATTTTGACATGATTAAGACCCCTCTGTACATGAAGCCTGGCAAGAAC	422
DB	487	TGGCAACCCCTTTTATTTTCACTGACCATGGAATATTCATGAACAATTCAAGA-----	541
QY	423	GCTCATATTTAATCATGATAGGGAAGGAAAGCTGAAACCTATGAAGAGTATACAGTG	482
DB	542	-----ACATTAGAGATCCCAAGGAGGGAACATATCTCATTTTCAAGGAAATATCCGCTG	597
QY	483	TACAGCAAGGAAGAAAGCGAGAGCTTCATTTCTAATAATTTGTTCGCCCATCCAG	542
DB	598	CTTTGCTTCAAATTAATCTGGGAATGCTATGTTCAGAGAAATAGAAATTTATAGTCCAAAG	657
QY	543	ATCACCATTTGTGACCAAGAAAGAAACCTTGAAACCAATCACTTCAAAGTGTCACTTTT	602
DB	658	TGTTCCAAATTTCCCAAGAAAGAAATTAATGACCTCTTGAAATGTGAGAGGAGATCCAAAT	717
QY	603	AGTACTTCCCTGCAAGACCCCAATTTGATTAACACACTATTAATTTTGGATGATTA	662
DB	718	TGTCCTCCCAATGCAATCTTCCCAAGGCTCCCACTTTTACAAATTTTGTATTAATAT	777
QY	663	TTCCCTTCAAAGACTTCCAAAGTAGAGAGTTTCTCAAGGTTTGAATGGGGAACCTTTA	722
DB	778	TGAATTTGAACACATGAAACAGATTAAGATTAATCATGACCCAAAAGGAGATCTATA	837
QY	723	TTTTTCCAAATGTCTCCCAAGAGACCCCGCAAGATATATCTGTATGCTGAATTTAA	782
DB	838	CTTTCGAAAAGGTGAGAAAGAAAGGACAGTGCATATGATCTATCTGTCTTTCGTCGATTTCC	897
QY	783	TCATACTCAACCATACAGCAAGCAACCTTATTTCTGTGAAGGTGATTTCACTGATGA	842
DB	898	AAGATTGAAGCATATTGTACAGAAATGCAATGAATGAATCAATGAATTAACATTTAAACA	957
QY	843	ATTGAATGACATATAGCTGTATTTTGATGACACTGATGTTTATTTGGTGCAATTAATCAG	902
DB	958	TGCTATATGATCAAGTTTCATCCACAGAAATTTGTTTCAAGGCAATTTCCATCAACGAAAG	1017
QY	903	TAGAGAGAGCCCAACCAATTTTAACTCCAAAGCAATGCAAGTAACAAAGAGAAAT	962
DB	1018	AAAAACCAAACTGCTGTGCTCCCTCCACCTGAGAGTGCGAGTGTCTTCAATTAACATCCT	1077
QY	963	AAAGAGAAATGTGCTTCACTGAGTGCAATTCAGAAAGACTGCTTACCCCAATTAATTTA	1022

Db	1078	C A A A G G G A A A T C T T G C G C T T G A G T G T T T T G C T G A A G C T T G C C A C T C C A G A G T T G A	1137
Qy	1023	C T G G C A A G A G A G T G G A A T G C T A C C C A A A A C A G A C A G T T A T A G A A C T T T G A G A A	1082
Db	1138	T T G G A A C A A A A T T G G T G G A C T T A C A A A G G G A G A G A C A A A A G A A A A T T A T T G C A A	1197
Qy	1083	A A C T T G C A G A T C A T T C A T G T T T C A G A A G C A G A C T C T G S A A T T A C C A A T G T A T A G C A A	1142
Db	1198	G A C T T T G A A G A T A G A A A T G T C T C C A C A G A C A A A A G A A A T T A T G C T G C A C A G C A G	1257
Qy	1143	A A A T G C A T T A G A G C A T C C A C C A T A C C A T T T C T T G A G T T T A A A G G G C T C C A T A C T G	1202
Db	1258	C A A T T T C T T G G A A C A G C C A C T C A C G A T T T T C A G T T A T A G T A G A A G C C T C T C G C G T	1317
Qy	1203	G A T C A C A G C C C C T C A A A A T C T T G T G C T G T C C C A G A G A G A T G G A C T T G A T C T G C A G	1262
Db	1318	G A C A A A A A G C C T C A G A G T G C G T A T A G A C C G G A A G C A A T G G C A T C T T G T A T A T G A	1377
Qy	1253	A G C T A T G G C A A C C C C A A A C C C A G A A T T A G C T G T T A A C A A T G A G T C C C A A T A G A A T	1322
Db	1378	G G C T A A A G A G A A C C T C A A C C C A C A T C A A G T G A G A C T A G C A T G C C C A G T G A C A A	1437
Qy	1323	T G C C C C A T A T G A C C C C A G A A A A A T A G A T G G C G A T C A A T T A T T T T T C A A A T G T T C A	1382
Db	1438	T C A T C A A T T T G - - C T G T G A T G T T G C T T C C C A G G A A A T C A G T T T T A C C A A C T T T C A	1494
Qy	1383	A G A A A G A T C A A G T G C A G T A T A T C A G T G C A A T G C C T A T A G A A T A T G A T A T T T A C T G C	1442
Db	1495	A C C A A T C A T A C T G C T G T G T A C A G T G A A G C C T C A A A T G T C A A T C A T G A A C T A T C C T T G C	1554
Qy	1443	A A A G C A T T T G T A A T G T G T G C T G A G C A C C A G A A T C C T C A C A C C T G C A A A C A C A C T	1502
Db	1555	C A A T C C A A T A T T G A T G T T G T G A A T G T C C G T C A T T G A T A C A A C C A A A G A T G A G A A A	1614
Qy	1503	C T A C A G G C A T T G G A A A C A G G C C G C T T T A C T A C T G T G C T T T G A G T C C T C C T	1562
Db	1615	T T A C C C T A C A G T G T T G G G T A C A G T G C T T T C T T A C A T T G C A G A T T C T T T G C T C A C T G A	1674
Qy	1563	C C C A A C C A T C G A T G G T T T T A A A G A G C T A A A G A A G A G T C C T C T C A T G A A G A T A T T A T G T	1622
Db	1675	G G C A C T C G T C T C T G C A G A A G T G A A A G A A G T G A A C C C T G A G G G C A A G C G T A T C A	1734
Qy	1623	T T T A C A T G A A A A T G A A C T T T G A A A T C A A A G A T C T A C A T G A T C G T T A A A G A A A T T C C	1682
Db	1735	T A T C A T A G A A A T G G C A C A T T G C A T G A T C A A C A G A C A C C G A A G A A G T C G G G T C T T A	1794
Qy	1683	T G T G G C C C A A A A G A C A G T A C A G A A C T T A T C T G T G T T G C A A G A A T A A A T T A A G G A T	1742
Db	1795	C T C A T G T T G G G T A G A A A A T G C A T A T G A A A A A C T C A G T C A C A G C C A A T T T G A T A T T A G	1854
Qy	1743	G G C A A A G A T A G A A G T T C A C T T A C A C C C G A A T A T G C A G T G T G C A A A A G G A G A C A T G T	1802
Db	1855	A A A T G C T A C A A A C T T A G A G T T T C T C T A A G A A T C T G T A T C C C A A A T T G C A T A T C T	1914
Qy	1803	G T C C T T T G A A T G C A A A G T G A A A C A T G A T C A C A C T T A T C C T A C T G T C T G T G G C T G A A	1862
Db	1915	T G A A T T A C A T G T G A A A G C A A A T G T G A C T C A C A T T T G A A A C A C A G T T T G A A G T G T C T G	1974
Qy	1863	G G A C A A C A G G A A C T G C C C A G T G A T G A A A A G T T C A C T G T T G A C A A G A T C A T A G T G T	1922
Db	1975	G A G T A A A G A T G A A A G C C T T T G A - - - A A T T A A T G C A C A G A A A T G A G C A G A T	2025
Qy	1923	A C C T A T A T G C A T G A C G A T A C A G C G G A C C T A C A C G T G T G G C C A C A C A C A C A C T C T G A	1982
Db	2026	A A T T A T T A T G A G A G C T A A T T T A C A T A T C T A A T G A A C T T T A G A G G A C A A G A T A T T T A	2085
Qy	1983	C A G C G T C T C C G C A G C G C T G T G C T T A G C G T T G C T C T A C T C C A A C T C A G C T C C G T	2042
Db	2086	C T G C T G T T C A G C T C A T A C T G C T A G A C A G T C G C G C A T A - - - T A C T C A A G T A A C T G T	2142
Qy	2043	T T A C A A T G T C C C A A A T C T C C C T T T G A C T T A G A C T G A C A G A T C A A C T T T G A C A A A A G T	2102
Db	2143	T C T T A T A T G T T C C G A T T C C A C A A A A C C T T C A C T T G C T G A A A C A G A A C A G A A G T	2202

QY	2103	TCAGCTGTCATGAGCCCCAGGCGATGCAACAATAGCCCATTTACAAAATTGTCATGCA	2162
Db	2203	TCGGCTGACCTGGGAGACTGGAGCTGACCAACAACAGCAATATTAGCGATATATTGTGA	2262
QY	2163	ATTATGAGATGCATATGACACAAGCCAGGGCTGTGGCAACAACAACTGAATTTCTGGAAC	2222
Db	2263	ATTTGAGAGAAACAAGAGAGCTTGGAGGTGGAGAACTGACACGATCTCCAGGGAAA	2322
QY	2223	ACAGACCAAGCCCCAGCTGAAGCTGTCTCTTACGTGACTACTCTTCCGCGTATGCG	2282
Db	2323	GAAAACCAAGTTATCTTACCTTTGGGCTCCATTGTGATATACAGTTCAGGGTCATAGC	2382
QY	2283	AGTAAACAAGCTTTGGGAAAGCTTGGCCAGGAGGGCTGAGCAGATTTGACGAAGC	2342
Db	2383	CGTGAACAGATAGGAGAGAGATCAGCCTTACGACCCCTGACACATATGAAACACACC	2442
QY	2343	CTCAGAACCAAGTAAAAACCCACAGCTGTGGAAGACTGGGATCAGAGCCTGATATATTT	2402
Db	2443	AGCAGCTCCAGATTTGGAATCCACAAAACATTAAGGGTTCAAGCCTTCACCCAAAGAAAT	2502
QY	2403	GGAAGTTACGTGGAAGCCCTTGAATGGTTTGAATCTAATGGGCGAGCCCTTAGTACA	2462
Db	2503	GATTATAAAGGGAGGCGCTTTGAAATCCATGAGACAGAAATGAGACAGGCTTAGAGTACAG	2562
QY	2463	AGTTAGCTGGGCGCAGAAAAGATGTGTGATGATGAAATGACATCTGTGGTTGTGCAATGT	2522
Db	2563	AGTGAACCTGGAAAGCCACAGGGAGCCCAAGTGGATGGGAGGAAGAAACAGTCAAAACC-	2621
QY	2523	ATCCAAATATATTGTCTTCAGGACGCGCAACTTTGTTCCATCCTGATCAAAGTTACAGC	2582
Db	2622	--ACACATTTGGGGTGTATGACGCTGTGTCATGACCCCTTAATGATGTCAAAGTCCAGGC	2679
QY	2583	CGTGAATGACATGGGGTGTGGCCCCGAGCCAGCTGTATGATGGGACATTTCTGGAGAGA	2642
Db	2680	TATCAATATACATAGATATCGGGCTGACCCCTGACCTCAGTCACTGACTCTCTATTTCTGGAGAGA	2739
QY	2643	CCTCCCAATGTGTGCTCCTGGGAAAGTGCCTGTGATGTGGTGAACAGTACCTTACCGCA	2702
Db	2740	CTATCCTGATACAGCTCCAGTGATTCATGGGGGTGAGGTTATAAACAGTACATTAGTTAA	2799
QY	2703	GGTGACCTGGGACCCAGTACTCTGGAAGAAGATCCGAGGACACTTAAGGCTATCGGAT	2762
Db	2800	AGTTAACCTGGTCAACAGTTCCAAAGGACAGAGTACATGACGTTCTGAAGGCTATACGAT	2859
QY	2763	TTACTATTGGAAGAACCCAGAGTTTCATCTTAAAGAAACAGACGTACATTGGAAGAAAGAT	2822
Db	2860	AAATTGTGTGGAAGAAACAABAATCTGTGTGGATGGAGAAACATCTCCAAAGAGTGAACAT	2919
QY	2823	CCTCACTTCCAGGCGAAGACTCATGTGCATGTGGCGGGCTAAGGCCCTTTAGCCA	2882
Db	2920	TCTAAGATTTTCAGGACAAAGAAACTCTGGAGATGTTCTTCTCTTAAGATGCTTTATGTGA	2979
QY	2883	CTACACACTGATGATGCGAGTGTGCATATGGGAAAGGGAGGGGCCACAGCCCTTGACAG	2942
Db	2980	ATTTTATTTAAACAGTCTTAGCTTACCTTAACTCTTAAAGAGCTGTGCTGAAAGTGACCTTA	3039
QY	2943	AGTCTTTATATCTCCAGAAAGAGTCCCAAGTGCCTCGTCTTTGAAGATTGTGAATCC	3002
Db	3040	TATATTTTCAAAACAACAGAAAGAGTACCTGAACACGCCAACTTTTCTAAAGGTCATCAAGT	3099
QY	3003	AACACTGGAATCTCTCACTTTGGAAATGGATCCACGAGCCACCGGAATGGCATTTTGAC	3062
Db	3100	TGATTAACAACACTGCACTTTATCTTGGGGGACTACTTAAGAAATTTAAATGGAACCTTAAC	3159
QY	3063	AGAGTACACTTTAAAGTATCAGCAATTAACAGACACATGAATTAAGGCCCTCTGTATGA	3122
Db	3160	TGGCTATCTTTTGGCAATTCAGATATATAAATGACACCTAGAGATTTGAGAAATTAATGA	3219
QY	3123	TTTGAAGAAAT--CCTGCCAACAAGACACGGTGAATTTTAAATAATTTTACAGCAC	3179
Db	3220	TATTAACATTTCAACTCCATCAAGGCCAGCTGGCACTCTTCAAACTGATGCAACTTAC	3279

QY 3180 TCGATTAAGTTTATTTCTATGACAAATCATGAGATGATGAGAAATCAATTACAGA 3239
 DB 3280 CAAGTCAATTTCTACTTGAAGGCTTGACCTTCACAGGGCTGTGAAAAACCATTCAGGA 3339
 QY 3240 GGAA 3243
 DB 3340 GGAA 3343

RESULT 5

US-10-435-751-153
 ; Sequence 153, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Chailita-Eid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; TITLE OF INVENTION: Entitled 282P163 Useful in Treatment and Detection of Cancer
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 153
 ; LENGTH: 7491
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-435-751-153

Query Match 11.4%; Score 472.8; DB 13; Length 7491;
 Best Local Similarity 48.8%; Pred. No. 1.1e-128;
 Matches 1467; Conservative 0; Mismatches 1507; Indels 30; Gaps 6;

QY 243 ACAGCCTCCACCATCACCACCAAGTCTCCAAAGATTACATTATTTGACCTCTGGAGAA 302
 DB 361 ACAGGTTCAACATATATATAAAGTCAAAAGTCCAAAGTTGCTTCCCTTGATGATGA 426
 QY 303 TATTTGATTCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTGACCCGTAA 362
 DB 427 TTTTCAAAATTTGATGAAAGTAAAGAAATCCAGAAACCAATTTTCTGGAATTAAGA 486
 QY 363 TGGGATCATTTTGCATGATTAAGACCTCTGTGCACATGAAAGCTGGACACGAAAC 422
 DB 487 TGGCAACCTTTTATTTTACTGACCATGATTAATTTCCATGAAACAAATTCAGGA---- 541
 QY 423 GCTCAATTAATTAATCATGATGAGAAAGGAAAGCTGAGACCTTAATGAAGAGTCTATCAGT 482
 DB 542 ----ACATTCAGATGCCAAAGAGGGGACATATCTCACTTTCAAGGAATATCCGCTG 597
 QY 483 TACAGCAGAAAGAAAGCGGAGCTGCAATTTCTAATAACATTTGTCGCCCATCCAG 542
 DB 598 CTTTGGCTTCAATTAATCTGGGAATGCTATGTCAAGAAATAGAAATTAATTAATTCAG 657
 QY 543 ATCACCATTTGTGAGCCAAAGAAATTTGAACCAATCAACATTCACAAAGTGTCAAGCTTT 602
 DB 658 TGTTCCTCAAAATTTCCAAAGAAATTAATTAATCTTGAATGAGAGAGGAGATTCAT 717
 QY 603 AGTACTTCCCTGACAGACCCCAATGATGATTAACCACTATTAATTTTGAATGATGA 662
 DB 718 TGTCTCTCCATGATCTCTCCCAAGGCTCCCACTTTACATTTATTTGATGAATAT 777
 QY 663 TTTCTTTCAAGATCTTCAAAAGTGAAGAGTGTCTCAAGTTTGAATGGGAGCTTTA 722
 DB 778 TGAATTTAGAACATGAAAGAAAGATGATATCATGAGCAAAAGGAGATCTATA 837

QY 723 TTTTTCATATGCTCTCCAGAGACACCCGACAGATATATCTGTATGCTAGATTAA 782
 DB 838 CTTCCCAACGTTGAAGAAAGGACAGTCCGAAATGACTATGCTGTGCTGCAATTTCC 897
 QY 783 TCATCTCAAAACATACAGCAGAGAACCTTTTCTGTGAAGTATTTTCAAGTGAATGA 842
 DB 898 AAGATTGAAGACTATTTGTAAGAAATATGCAATGAATCAATTAACATTTAAAGCA 957
 QY 843 ATTGAATGACACTATAGCTGCTAATTTTGAATGACACTGAGTTTATGAGTAAATCAAG 902
 DB 958 TGTCTAATGACTAATGATTCATCCAGAAATTTGTTTCAAGGAATTTCCATCAACAGAA 1017
 QY 903 TAGAGAGGCCCAACCAATTTTAACTCCAGAAAGCAATGCAATTAACAAAGAAAT 962
 DB 1018 AAAACCCAAACGCTGTGCTCCACAGAGAGTGGAGTGTGCTTCAATTAACATCCT 1077
 QY 963 AAGAGAAATGTGCTTTCACTGAGTGCATTTGACAGAGAGAGAGTGTCTTACCAATTTA 1022
 DB 1078 CAAGGGGAAATCTTGTGCTGATGATGTTTGTGTAAGGCTTGCACACCTCCACAGTTGA 1137
 QY 1023 CTGGGCAAGAGATGGAATGCTACCCAAAGAGAGAGTGTATTAAGACTTTAGAA 1082
 DB 1138 TTGGAACAAATTTGTGTGACTTACCAAGGGGAGAGAGCAAAATTAATGAGCA 1197
 QY 1083 AACCTTGAGATCATTTATGTTTCAAGAGAGAGTCTGGAATTTCAATGATATAGCAAA 1142
 DB 1198 GACTTTGAAGATGAGATGATGCTCTTCAAGAGAGCAAAAGAAATTTTCCCTGACAGCCAG 1257
 QY 1143 AATGCAATTAAGAGGATTCACATCAATTTCTGTGAAGTAAAGGCGCTCCATCTG 1202
 DB 1258 CAATTTCTGGGAACAGCACATCAAGATTTTCACTTATGAGAGAGAGCTCTGCTG 1317
 QY 1203 GATCACACCCCTCAAAATCTGTGCTGTCCCGAGAGAGATGGGACCTTATGTCAG 1262
 DB 1318 GACAAAGAGGCTCTGAGAGTGTGTATAGCAACCGGAAGCAATGCACTGTGTATGGA 1377
 QY 1263 AGCTAATGCAACCCCAACCCAGATTAAGTGTGTTAACAATGAGAGTCCCAATGAAT 1322
 DB 1378 GGTGAAGAGAGAGCTTCAACCAATCAATGAGAGATGCAATGCTCCCAAGTTGACAA 1437
 QY 1333 TGGCCCTGATGACCCGACAGAAATTAAGAGGAGATCAATTTTTCATATGTTCA 1382
 DB 1438 TCATCATTTTG--CTGGTATGTTGTCTTCCCGAGGAATCAAGTTTATCAACCTTCA 1494
 QY 1383 AGAAGATCAAGTGAATATATGATGCAATGCTCTTAATGAATATGATATTTCTGGC 1442
 DB 1495 ACCAATATATCTGTGTGTACAGTGTGAAGCTTCAATGTCCATGGAATCTATCTTGC 1554
 QY 1443 AAAGCATTTGTAATGTGCTGCTGAGCCACAGATCTTCAACCTGCAACACT 1502
 DB 1555 CATGCAATATGATGATGTTGTGATGATGCTGCTCAATGATCAACCAAGATGAGAA 1614
 QY 1503 CTACAGGTCAATGGAACAGGCTCTTATCTAATGATGCTTTTGGGTCTCTCT 1562
 DB 1615 TTAGCTACAGTGTGAGTGAAGTGTGCTTCTTCAATGAGAGTCTTTGCTTCACTGA 1674
 QY 1563 CCCAACAATGAGTGTGTTAAAGAGCTTAAGAGAGTCTTCTCATGAAGATTTATGT 1622
 DB 1675 GGCAGTGTGTCTTGGCAGAAAGTGAAGAGTGAACCCCTGAGAGGAGCGGTATCA 1734
 QY 1623 TTTACATGAATATGAACTTTGGAATCAAAAGATGCTATGATGTTTAAAGAAATCC 1682
 DB 1735 TATCTATGAATATGCAATTTGCAATCAAGAACCAAGCAAGATGCTGGTCTTA 1794
 QY 1683 TGTGCCCCAAAGACAGTACAGAACTTATAGTGTGTTCAAGAAATTAATAGGAT 1742
 DB 1795 CTCATGTTGGGAGAAATATGCTATAGAAATATGCAAGTCAAGCAATTTGATATAG 1854
 QY 1743 GGCAGAGATGAGTTCATTAACGCGGAATATGCAATGCTGTCAAGAGAGAGATGCT 1802
 DB 1855 AATGCTCAAAATCTTAAGATTTCTCTTAAGAAATCTGTATCCCAATTTGCAATATCT 1914
 QY 1803 GTCTTTGAATGCAAGTGAAGATGATCAACCTTATCCCTCACTGTCTGTGCTGAA 1862

423 GCTCATATTAATCATATGAGCGAAGGAAAGCTGAGACCTATGAGAGTCTATGAGT 482
462 ----ACATTCAGAGATCCCAAGAGAGGAGCAATATCTCATCTTCAAGGAAATACCGCTG 517
483 TACAGCAAGAAAGAAAGCGAGAGCTGCAAGTTCTTAATTAACATTTGTCGCCCATTCAG 542
518 CTTTGGCTTCAAAATTAACCTGGGAATCGCTATGTCAGAAAGAAATGAATTTATAGTCCAG 577
543 ATCACCATGTGAGCCAAAGAAAATCTTAACCAATCACACTTCAAGAGTCAAGCTTT 602
578 TGTTCAAAATCTCCAAAAGAAAAATGACCTCTTGAAGTGAAGAGAGAGATCAAT 637
603 AGTACTTCCCTGAGAGACCCCAATGATTAACACCACTTAATATTTTGAATGATGA 662
638 TGTCTCCCATGGAATCTTCCAAAGCCTCCACCTTTACATTTATTTGATGAATAT 697
663 TTTCTTTCAAAAGATCTTCAACAAAGTGAAGAGTTCTCAAGTTTGAATGGGAGCTTTA 722
698 TGAATTTAGAAACATGGAACAGATGAAGATATCATGAGCCAAAAGGAGATCTATA 757
723 TTTTTCATGTCTCCCAAGAGACCCGCGAAGCTAATCTGTATGTATGATATTA 782
758 CTTTCGAAACGTGGAAGAAAGAGAGCTGCAATGACTATGCTTGTGCTGCAATTTCC 817
783 TCATACTCAAAACCATACAGACAGAGCAACCTATTTCTGGAAGTGAATTTCAAGTGA 842
818 AAGATTAAAGACATTTGTACAGAAATGCAATGAATCTAACAGTTTAACAGTTTAAGCA 877
843 ATTGAATGACACTATAGCTGTAAATTTGAGTGAAGTGAATTTATGCTTAATCAAG 902
878 TGTATATGACTCAAGTTTATCAAGAAATTTGTTCAAGGCAAAATTCATCAAGCAAG 937
903 TTAGAGAGAGCCCAACATTTTAACTCCAGAAAGCATGCAAGTAACAAAGAGAAAT 962
938 AAAACCCAACTGCTGTGCTCTCCCAAGAGTGAAGTGAATTTCAATTAACATCTCT 997
963 AAGAGAAATGTGCTTTCACTGAGAGTCAATGCAAGAGAGCTGCTTACCCCAATTTTA 1022
998 CAAGAGGAAATCTTCTGCTGAGTGTGTTTGTGAGAGCTTCCCACTCCACAGTTGA 1057
1023 CTGGGCAAAAGAAATGAAATGCTTACCAAAAACAGAGACGTTTATGAACCTTTGAGA 1082
1058 TTGGAACAAATTTGTTGAGTGTACCTAACAAAGGAGAGAAACAAAGAAATTTATGGCA 1117
1083 AACCTTGCAGATCATTTATGTTTCAAGAGACAGCTTGAATTTACATGTAAGCAAA 1142
1118 GACTTTGAAGATGAAGAAATGCTCTTACCAAGAGCAAAAGAAATTTATGCTGACAGCCAG 1177
1143 AAATGATTAAGAGCATCACCAATATCATTTCTGTTAAGTTAAAGGGCTCCATATCTG 1202
1178 CAATTTCTTTGGAGAACGCACTCAAGATTTTCAAGTTATGTAAGAGAGCTCTCGCTG 1237
1203 GATCAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGAGTGGAGCTTATCTGAG 1262
1238 GACAAAGAAAGCTCTAGAGTGTGTATAGCACCGGAACCAATGGCATTTGTATGTA 1297
1263 AGCTAATGGCAACCCCAACCCAGAAATTAAGCTGTGTTAACAATTGAAGTCCCAATAGAAT 1322
1298 GGTAAAGAGAGAACTTCAACCAATCAAGTGAAGAGTCAATGTGCTCCCAAGTTGACAA 1357
1323 TGCCTTGAAGACCCAGAGAAAATAGATGGCGATACCATTAATTTTCAAAATGTTA 1382
1358 TCATCATTTTGG--CTGTGATGTTGTCTTCCCAAGGAAATCAGTTTATCAAACTTTCA 1414
1383 AGAAAGATCAAGTGAATATATAGTGAAGTCACTTAATGAATATGATATTTATCTGCG 1442
1415 ACCAAATCATCTGCTGTGTACAGTGTGAAGCTTCAATGTTCATGGAATCATCTTCC 1474
1443 AAAGCATTTGTAATGTCTGCTGAGAGCAACGAATCTTCAACACTGCAAAACACT 1502
1475 CAATCCAAATATTTGTTGTGATGTCTGCTCATTTGATTAACAAACCAAGATGAGAGAA 1534

1503 CTACAGGTCATTTGAAACAGGCTGCTTTACTAGACTGTGCTTTTGGGTCTTCTCT 1562
1535 TTACGCTACAGTGTGTTGGGTACAGTGTCTTTTCAATTTGCAAGTCTTTGCTTCACTGA 1594
1563 CCCAACATGAGTGTGTTTAAAGAGCTTAAGAAAGTGTCTTTCAATGAAGATTTATATG 1622
1595 GGCAGTGTGTCTGCAAGAGAGTGAAGAGTGAACCCCTGAGAGGAGCGGTATCA 1654
1623 TTTACAGAAATGGAACCTTGAATCAAAAGATGCTATCATGAGATGTTTAAAGAAATTC 1682
1655 TATCTATGAATATGACATTCAGATCAAGAAACACCCAGAAAGATGCTGGCTTTA 1714
1683 TGTGCGCCAAAAGACAGTACAGAACTTATACGTGTGTGCAAGAAATTAATTTGGAGAT 1742
1715 CTATGTTGGGTAGAAAATGCTATAGAAAACCTGCAAGTCAACAGCCAAATTTGATATAG 1774
1743 GGCAAAAGATGAAGTTCACTTACAGCCGAATATGCAAGTTGTGCAAAAGAGGAGCATGT 1802
1775 AATGCTACAAAACCTTAAGATTTCTTAAAGATCTGTATCTCCAAATTTGCAATATGCT 1834
1803 GTCTTTGAATGCAAGTGAACATGATCACCTTATCCCTACGTCTGTGGCTGAA 1862
1835 TGAATTTACTTTGTAAGCAATGTGACTCACATTTGAAACACAGTTTGAAGTGTCTCG 1894
1863 GGACAAACAGGGAATGCGCAGATGAAGAAAGTTTCACTGTGACAAAGATCATCTAGTGT 1922
1895 GAGTAAAGTGAAGAGCTTTGA-----AATTAATGAGCAAGAAAGATGGCAGAT 1945
1923 AGCTAATGCTAGTACATGATGACAGCGGAGCTTACAGTGTGTGCAACCACTCTGGA 1982
1946 AATTATTTAGTGAAGCTTAATTTGACCATATCTAATGTAATTTAGAGAGCAAGATATTTA 2005
1983 CAGGCTTCCGCAAGCTGTGCTTAAAGGTTGTGCTCTTCTACTCAACTCCAGCTCCGT 2042
2006 CTGCTGTACGCTTACCTGCTTACAGAGTCTGCGATA--TACTCAAGTAACTGT 2062
2043 TTACAGATGCCCAATCTCTCTTGAATGAACTGACAGATCAACTTGAACAAAGTGT 2102
2063 TCTTGAATGTCCGATTCACACAGAAACCTTCACTGTGTGAAGACAGAAAGAGTGT 2122
2103 TCACTGTCAATGACCCCAAGGATGACAAATATGCCCCATTTACAAATTCATATGCA 2162
2123 TCGGCTGACCTGGGAAGCTGAGCTGACACCAACAGCAATTTTACCGATATATTTGTA 2182
2163 AATGAAGATGAATGACCAAGCCAGGCTGTGAGACCAACAAATGAAGTTTCTGGAAC 2222
2183 AATTGAAGAAACAAAGAGAGCTGGAAGTGGAGGAATGACACAGATCCAAAGAA 2242
2223 ACAGACCAAGCCAGCTGAAGCTGTCTCTTACGTGAATCACTCTTCCGGGTATGGC 2282
2243 GAAACCAAGATATCTTATCTTTGGCTTCATTTGTGATACAGATTCAGGCTATAGC 2302
2283 AGTGAACAGATTGGGAAGAGCTTGGCCAGAGGCGTGTAGAGATATTTGACAAAGC 2342
2303 CGTGAACGAAGTGAAGAGAGTCAAGCTTACAGCAGCGCTCAACATATGAACACCAAC 2362
2343 CTGCAACCAAGATTAACCCCAAGCTGTGGAAGAGATGGAGTCAAGAGCTGATATTT 2402
2363 AGCAGCTCCAGATGAAGATCAACAAATTAAGGTTTAAAGCTTCTCAACCAAGAAAT 2422
2403 GGAGATTTAGTGAAGAGCTTGAATGTTTGAATCTAATGGGCAAGGCTTCAATAGCA 2462
2423 GATTTATTAAGTGAAGCTTTGAAATCAATGAGAGAAATGACCAAGGCTTGAAGTACAG 2482
2463 AGTTAGCTGGCGCCAGAAAGATGATATGATGAATGACATCTGTGTGTGGCAATGT 2522
2483 AGTGACTGGAAGCCACAGGAGCCCAAGTGAAGTGAAGAAAGAAACAGTCAACAAAC 2541
2523 ATCCAAATATATGTCTCAGAGCAAGCCAACTTTGTTCCATACGATCAAAAGTTCAAGC 2582
2542 --ACATTTGGGGGTATGAGCGCTGTCTATGCTTATGATGTCAAAGTCCAGGC 2599
2583 CCGAATGACATGGGGTTTGGCCCGAGCCAGCTGTATGTCATGGGACATTTCTGAGAAAG 2642

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Db      2600 TATCATCACTAGATGATCGGCGCTGACCTCAGTCAGTACTCTCTATTCTGGAGAGAA 2659
QY      2643 CCTCCCAATGATGCTCTCTGGGAAAGCTGGTGTGAATGTGTGAACATGACCTTAGCCGA 2702
Db      2660 CATATCTGTAGACAGCTCCAGTAGTCCATGGGGTGGAGCTTATTAACAGTACATTAATTAA 2719
QY      2703 GGTGACCTGGAGCCAGTACCTCTGAAAAGATCCAGAGACACTTCAAGAGCTATCGAT 2762
Db      2720 AGTTACTCTGTCAACAGTCTCAAGAGACAGAGTACATGACGCTGCAAGAGCTATCAGAT 2779
QY      2763 TTAATATGAGAGACCCAGAGTTCATCTAAGAAAAGAGAGCTGACATTTGAGAAAAGAT 2822
Db      2780 AATATGCTGAGAAAAGAAAAGTCTGTGGATGAGAAACATCCCAAGAAAGTGAACAT 2839
QY      2823 CCTGACCTTCCAGAGAGAGACATGACATGTCGCGGGCTTAGAGCCCTTAGGCA 2882
Db      2840 TCTAAGATTTTCAGGACAAAGAACTCTGGATGTTCTCTCTTAGATGCTTTAGTGA 2899
QY      2883 CTACACACTGAATGTCCGAGTGGTCAATGGGAAAGGGAGGCGCCAGCCGCTGACAG 2942
Db      2900 ATTTCATTTAAGCTCTTTCAGCTATTAATCTTAAGAGAGCTGTCTGAAAGTGAAGCTTA 2959
QY      2943 AGTCTTTAATPACTCCAGAAAGAGTCCCAAGTGTCTCCCTGCTTGAAGATTTGTAATCC 3002
Db      2960 TATATTCAAAACAGCAAGAAAGAGTACCTGAACAGCACTTTTCTAAGATCATCAAGT 3019
QY      3003 AACACTGGAGCTCTCTCACTTTGGAATGGATCCACGAGCCACCCGAATGGCATTTTGAC 3062
Db      3020 TGATTAAGACACTGCGCACTTTATCTTGGGAGACTAAGTAAAGTAAAGTAAAGCTTAAC 3079
QY      3063 AGAGTACACTTAAAGATATCAGCAATTAACAGACACATGATTAAGCCCTCTGTGTAGA 3122
Db      3080 TGGCTATCTTTTGCATATACATTAATTAATGACACTAGAGATTGGAAATTAATGA 3139
QY      3123 TTTGAAATTT---CCTGCCAACAAGACAGGTGACTTTAAATTTAATTTAGACAG 3179
Db      3140 TATTACATTAACAATCCATCAAGAGCCAGCTGACCTCTCAAACTGAATGACATAC 3199
QY      3180 TCGATTAAGTTTATTTATTTCTATGCAACAAACATGAGAGATGAGAAATTAACAA 3239
Db      3200 CAAGTACAAATTTCTACTTGAAGGCTTGACCTTACAGGGCTGTGAAAAACGATCAGGA 3259
QY      3240 GGAA 3243
Db      3260 GGAA 3263

RESULT 7
US-10-435-751-193
; Sequence 193, Application US/10435751
; Publication No. US2004005348A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Fairle, Mary
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Jakobovits, Ava
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; FILE REFERENCE: 5158-20084.00
; CURRENT APPLICATION NUMBER: US/10/435,751
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 7570
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-435-751-193
Query Match      11.4%; Score 469.6; DB 13; Length 7570;
Best Local Similarity 48.8%; Pred. No. 1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

QY      243 ACAGCCTCCAAACCATACACCCCAAGTCTCCAAAGATTATTAATTTGACCTCTGGAGAA 302
Db      287 ACAGGTTCCAAACATATCAATTAACAGTCAAAAGTCCAAAGTGGCTTCCCTTGATGATGA 346
QY      303 TATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTTGGACCCGTAA 362
Db      347 TTTTCAAAATGTGAATGAGCTAAAGGAAATCCAAACCAATTTTGTGTGACATMAGA 406
QY      363 TGGGACTATTGTGACATGATTAAGACCCCTGTGTCACATGAAAGCTGGACAGAAAC 422
Db      407 TGGCAACCTTTTATTTTCACTGACATCGATGATTAATTCATGCAACATTCAGGA----- 461
QY      423 GCTCATTAATTAATCATATGAGGAGGAGAAAGCTGAGACTATGAAAGAGTCTATCAGTG 482
Db      462 ----ACATTCAGGATCCAAACGAGGGGCAATATCTCATCTTCAAGGAAATACCGCTG 517
QY      483 TACAGCAAGAAAGCAACGCGAGCTGCAAGTTCTAATAACATGTTGTCGCCCATCCAG 542
Db      518 CTTTGCCTTCAATATAAATGCGGATGCTATGTCAGAAAGAAATAGATTAATAGTTCAGAG 577
QY      543 ATCACATTTGTGAGCAACAAAGAAACCTGAACCAATCACACTTCAAAATGTGCAAGTCTTT 602
Db      578 TGTTTCAAAACCTCCCAAAAGAAAGAAATGAGCTCTTGAAGTGGAGGAGATCCAAAT 637
QY      603 AGTATCTCCCTGACAGACCCCAATTTGATTAACACACCTATTAATTTTGGATGATTA 662
Db      638 TGTCTCTCCATGCAATCTCTCCCAAGGCTCCACCTTTAACAATTTATGATTAATAT 697
QY      663 TTCTTTCAAGACCTTCAAAAGTGAAGATTTCTAAGTTTGAATGGGACCTTTA 722
Db      698 TGAATTAAGAACATATGCAAGAAAGATGAATATATGAGCCAAAGGGAGATCTATA 757
QY      723 TTTTTCCAATGCTCCCAAGAGAGACACCGGAGAACATATATCTGTATNGCATTTAA 782
Db      758 CTTGCAAAACGTGAGAAAGAGACAGTGCATATGACTATGTTGCTTGTGCGCATTTCC 817
QY      783 TCATATCAAAACCATACAGACAGAAAGCACTATTTCTGTGAAGTGAATTTCAAGTGA 842
Db      818 AAGATTAAGACATATTTGAAGAAATATGCAATGAATCAAGTTAACAGTTAAAGCA 877
QY      843 ATTTAATGACACTATAGTCTGTAATTTGAATGACACTGATTTATGCTTAATCAAG 902
Db      878 TGTCTATGACTCAATGATTCACAGAAATGCTTCCAAAGCAAAATTCATCAACCAAG 937
QY      903 TAGAGAGAGCCACCAACATTTTAACTCCAGAAAGCAATGCAAGTAAACAAAGAGAAAT 962
Db      938 AAAACCCCAATCGCTGTGCTCCCTCCACTGAGAGTGGAGTGTCTTCAATTAACATCCT 997
QY      963 AAGAGAAATGTGCTTTCACTGAGAGTGAATGCAAGAGACTGCTTACCCCAATTAATTA 1022
Db      998 CAAGGGGAAATCTTGCTGTGATGATGTTTGTGTAAGGCTTGCAACATCCACAGTTGA 1057
QY      1023 CTGGCAAGAGAAATGGAATGCTAACCAAAAAAGCAAGTTTAAAGAACTTTGAGAA 1082
Db      1058 TTGGAACAAATTTGTGTGACTTACCAAGGGGAGAGAAACAAAGAAATTAATGAGCA 1117
QY      1083 AACCTTGACATCATTTATGTTTGAAGAGACACTGTGAATTAACATGATATGCAAA 1142
Db      1118 GACTTTGAAGATGAGAAATGTCTCTACAGAGCAAAAGAAATTAATGCTGACAGCAG 1177
QY      1143 AATGATTAAGAGGCAATCAACCATATCTTCTTGAAGTAAAGGGCTCATTAAGT 1202
Db      1178 CAATTTCTTGGAGAAAGCACTACGATTTTACGATTAATGAGAAAGGCTCTCGCTG 1237
QY      1203 GATCAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGACCTTGATCTGAG 1262
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Db 1238 GACAAAGAAAGCTCAGAGTGTGTATGACACCGAGAACATGGCATCTTGTATGTGA 1297
 Qy 1263 AGCTAATGGCAACCCCAACCCGAAATTTAGTGTATTAACAATAGAGTCCCATAGAAAT 1322
 Db 1298 GGTGAGAGAGAACTCAACCCCAACATCAAGTGAAGTCAATGCTCCCAAGTTGACAA 1357
 Qy 1323 TSCCCCTGATGACCCCAAGAGAAATAGATGGCGATACCATTTATTTTCAAAATGTGA 1382
 Db 1358 TCATCATTTG---CTGGTGTATGTGTCTTCCCAAGGAAATCAGTTTACCAACTTCA 1414
 Qy 1383 AGAAGATCAAGTCAAGTATATCAATGTCATGCTCTTAATGAATATGATTTACTGGC 1442
 Db 1415 ACCAATCACTAGCTGTGTACAGGTGAAGCTCAAAATGTCCATATCTCTTC 1474
 Qy 1443 AAAGCATTTGTAATGTGTGGCTGAGCAACCAAGATCTTCACACCTGAAACACACT 1502
 Db 1475 CATATGCAATTTGATGTGTGTGTCCGTCCATTGATACAAACCAAGATGAGAGAAA 1534
 Qy 1503 CTACAGTCAATTCGAAACAGGCTGTCTTATCTAGCTGTCTTCTTGGGTCTCTCT 1562
 Db 1535 TTACGCTACAGTGTGGGTAGAGTCTTCTTCAATGCGATTTCTTGGCTTCACTGA 1594
 Qy 1563 CCCAATCAAGTGTGTTTAAAGAGCTTAAAGAGTCTCTTCAATGAATATTTATGT 1622
 Db 1595 GGCAGTGTGTCTGTGAGAGGTGAGAGTGAACCCCTGAGAGGCGAGGTATCA 1654
 Qy 1623 TTATACATGAATGAAGCTTTGGAAATCAAGATGTATAGATGATGTTAAAGAAATTC 1682
 Db 1655 TATCTATGAATTTGGACATTTGAGATCAACAGAACACCAAGAAAGATGCTGGTCTTA 1714
 Qy 1683 TGTGCCCCAAAGACAGTACAGAACTTATACGTGTGTGCAAGAGATTAATAGGAT 1742
 Db 1715 CTATGTTGGGTAGAAATGCTATAGGAAATCTGAGTACAGCCAAATTTGGATTTAG 1774
 Qy 1743 GCGAAAGATGAAGTTCATTAACGCCAATATGCAATTTGCAAGAGAGAGCATGT 1802
 Db 1775 AATGTCTACAAACTTAGAGTTCTCTTAAGATCTCTGATCCCAATTCATATGCT 1834
 Qy 1803 GTCTTTGATGCAAGTGAACATGATCAACCTTATCCCTCACTGTCTGTGTGTGA 1862
 Db 1835 TGAATTTACATGTGAAGCAAAATGTACTACATTTGAAACACAGTTTAAAGTGTCTG 1894
 Qy 1863 GGACAAACAGAGAACTGCCCCAGTATGAAGTTCATGTTGACAGAGATCATCTAGTGT 1922
 Db 1895 GAGTAAAGATGAGAAAGCTTTGA-----AATTAATGCGACAGAAAGTGGACAGAT 1945
 Qy 1923 AGCTATGTCAATGATGATGACAGCGGAGCTTACACGATGTGTGGCAACCACTCTGGA 1982
 Db 1946 AATTATTTGATGAGCTAATTTGACCATATCTAATGTATTAAGAGACCAAGTATTTA 2005
 Qy 1983 CAGCGTCTCCGCAAGGCTGTGTGTAGCTTGTGTCTTACTCCAACTCCAGCTCCGT 2042
 Db 2006 CTGCTGTTCAGCTCATCTAGCTCTAGACAGTGTCTGCCATTA--TAACTCAAGTAACTGT 2062
 Qy 2043 TTACAGATGCCCAATCTCTCCCTTTGACTTGAATCTGACAGATCAACTTGAACAAAGTGT 2102
 Db 2063 TCTTATGTCTCCGATCCACAGAAACCTTCACTTGTCTGAAGAGACAGAAACAGAGTGT 2122
 Qy 2103 TCAGCTGTCAAGACCCCAAGGATGACAAATAGCCCATTAACAAATTCATCATGCA 2162
 Db 2123 TCGGCTGACCTGGAGAGCTGGAGCTGACCAACAGCAATTTAGAGATATATTTGTTGA 2182
 Qy 2163 AATTAAGATGCAATGCAACAGCCAGGCTGTGCAACCAACTGAAGTTTCTGGAAC 2222
 Db 2183 AATTGAAGGAAACAAAGAGACCTGGAAGGTGGAGAACTGACCAAGTCCAAAGGAAA 2242
 Qy 2223 ACAGACCAAGCCCAAGCTGATGATCTCTTACGTAATCTATCTCTTCCGCTGATGGC 2282
 Db 2243 GAAACCAAGTATCTTACCTTGGCTCATTTGTGAATACACAGTTCAAGGTCTATAGC 2302
 Qy 2283 AGTGAACAGATTTGGAGAGAGCTTGGCCAGGAGGCTGTGACAGTATTTGACAAAGC 2342
 Db 2303 CGTGAACGAAGTAGGAGAAAGTCAAGCTTACGAGCGGTGACATCATGAACCAACCC 2362

Qy 2343 CTCAGAACCAATTAACAAACCCCAAGCTGTGAAAGAGCTGGATCAGAGCTGATTAATTT 2402
 Db 2363 AGCAGCTCCAGATAGAGATTCACAAACATAGAGTTCAAGCTCTCAACCAAGAAAT 2422
 Qy 2403 GGAGATTAAGTGAAGCCCTTGAATGTTTGAATCTAATGGCCAGGCTTCACTGACAA 2462
 Db 2423 GATTAATTAAGTGGAGCTTTGAATTCATGAGAGAGATGAGACAGGCTCTGAGTACAG 2482
 Qy 2463 AGTTAGCTGGCCCAAGAAAGATGTGATGATGAATGACATCTGTGTGTGGCAATGT 2522
 Db 2483 AGTGAACCTGGAAGCCAGAGGAGCCCAAGTGAAGTGAAGAAAGAACATCAAAACC- 2541
 Qy 2523 ATCCAAATATATTTGTCTCAGGACGCAACCTTTGTCCATCTGATCAAAAGTTCAAGC 2582
 Db 2542 --ACATTTGGGGATGAGAGCCCTGTGTCTATGCCCTTATGATGTCAAGTCCAGGC 2599
 Qy 2583 CCTGAATGACATGGGGTTTGGCCCGAGCCAGCTGTAGTCAATGGACATTTGAGAGAA 2642
 Db 2600 TATCAATCAACTAGGATCTGGGCTGACCTTCAGTCAAGTACTCTATTTCTGAGAGAA 2659
 Qy 2643 CCTCCCATGTGTGCTCTGGGAAGTGTGTGTGAATGTGTGAACATTACTCTTGCCGA 2702
 Db 2660 CTATCTGATACAGCTCCAGTATCATGGGGTGGACGTTTAAACAGTACATTAAGTTAA 2719
 Qy 2703 GGTGCACTGGGACCCAGTACCTCTGAAAGATCCGAGAGACCTTACAAAGGCTATCGAT 2762
 Db 2720 AGTTACCTGTGTCAAGATTCCTCAAGAGACAGATCATGAGCTGTGAAGGCTTACAGT 2779
 Qy 2763 TTACTATTGAAGAGCCAGAGTTCATCTTAAAGAAACAGAGTCACTTGAAGAAAGAT 2822
 Db 2780 AATTTGTGGAAGAACAAAGATCTGTGTGATGAAGAACATCCCAAGAAAGTGAACAT 2839
 Qy 2823 CCTACCTTCCAGGACAGACATCATGATGTGTGCGGGGCTAGAGCCCTTTAGGCA 2882
 Db 2840 TCTAAGATTTTCAGGACAAAGAACTCTGGAATGTGTCTTCTTGAATGCTTTTATGGA 2899
 Qy 2883 CTACACATGATGTCCGAGTGTGATGAGGAAAGGGGCGCAGCAGCCCTGACAG 2942
 Db 2900 ATTTATTTAAACAGTCTTAAAGCTTATACCTTATACCTTAAAGAGAGTGTCTTGAAGTGAACCTTA 2959
 Qy 2943 AGCTTTTAATCTCCAGAGAGATCCCAAGTCTCCCTGTCTTTGAAGATTTGTAATCC 3002
 Db 2960 TATATTTCAACACCAAGAGAGTACCTGAACAGCAACTTTCTTAAAGTTCATCAAGT 3019
 Qy 3003 AACACTGACCTCTCACTTTGGAATGGATTCACCGAGCAACCCGAATGGCATTTGAC 3062
 Db 3020 TGATTAAGACACTGACCTTATATCTTGGGAGCTACTTAAAGAAATTAATGAACCTTAAC 3079
 Qy 3063 AGAGTACACCTTAAAGTATCAGCCAAATTAACAGACACATGAATTAAGGCCCTGTGTGA 3122
 Db 3080 TGGCTATCTTTTGCATATCAGATTAATAAGACCTTACAGAGATTTGAATTAATGA 3139
 Qy 3123 TTTGAAATTT--CCTGCCAACAGACAGGCTGACCTTTAAATAATTTAAATTTGACAGC 3179
 Db 3140 TATTAACATTAACATCATCAAGCCAGCTGGAGCTCTCAAACTGATGACAACTAC 3199
 Qy 3180 TCGATTAAGTTTATTTCTATGCAAAACATCAGCAGATCAGAGTCAAATTTACGA 3239
 Db 3200 CAAGTACAAATTCATCTTGAAGGCTTGCACTTACAGAGGCTGTGGAAGAAACGATCACGGA 3259
 Qy 3240 GGA 3243
 Db 3260 GGA 3263

RESULT 8
 US-10-435-751-195
 ; Sequence 195, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Paris, Mary

APPLICANT: Challita-Bid, Pia M.
APPLICANT: Jakobovits, Aya
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Mangao
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 282p13 Useful in Treatment and Detection of Cancer
FILE REFERENCE: 51158-20084.00
CURRENT APPLICATION NUMBER: US/10/435,751
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 60/404,306
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/423,290
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 195
LENGTH: 7570
TYPE: DNA
ORGANISM: Homo sapiens
US-10-435-751-195

Query Match 11.4%; Score 469.6; DB 13; Length 7570;
Best Local Similarity 48.8%; Pred. No. 1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

243 ACAGCTCCCAACCATCACCACAGCTCTCCAAAAGATTACATTATTGACCTCGGAGAA 302
287 ACAGGTTCCACATCATATAAAGTCAAAAGTCCAAAGTTCAGTTCCTTCCCTTGATGAGTA 346
303 TATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTCGACCCGTAA 362
347 TTTTCAATTTGATGTGAAGCTTAAGGAATCCAGAACCAACTTTTCTGCTGACTAAGA 406
363 TGGGATCTATTGATGATGATTAAGCCCTCTGCTGACCACTGAAACCTCGACAGAAAC 422
407 TGGCAACCTTTTATTATTACATGACCATGGATTAATTCATGCAATTCAGGA----- 461
423 GCTCAATTAATCATCATGAGCGAAGAAAGCTGAGACCTTAATGAAGTCTATCAGT 482
462 ----ACATTCAGATTCACCAAGGAGGACATATCTCATCTTCAAGGAATACCGCTG 517
483 TACAGCAAGAAAGAAAGCGGAGCTGCAAGTTCTTAATTAATTTGTCGCCCATCAG 542
518 CTGTGCTCAATTAATCGGAAATCGCTATGTCAGAAAGAAATGAATTAATGATTCAG 577
543 ATCAACATGTGAGCAAGAAAGAAATCTTGAACCAATCACTCAAGTGTGATCAGTCTT 602
578 TGTTCAAAATCTCCAAAAGAAATTAAGACCTTGAAGTGAAGAGGAGATCAAT 637
603 AGTACTTCCCTGAGACCCCAATTTGATTAACACCACTTAATTAATTTGATGATGA 662
638 TGTCTCCCATGATATCTCTCCAAAAGCTCCCACTTTACATTTATTTGATGAATAT 697
663 TTTCTTTCAAGACTTCCAAAGTGAAGAGTTCCTCAAGTTTGAATGGGACCTTTA 722
698 TGAATTAGAACAATGAGCAAGATGAAGATATCATGAGCCAAAGGAGATCTATA 757
723 TTTTTCATGTCTCTCCAGAGACACCGCGGAAGCTATATCTGTATGCTAGATTTAA 782
758 CTTCGAAACGTGAGAAAGAAAGACAGTGCATGACTGTGCTGTGCTGATTTTC 817
783 TCATACTCAACCATGACAGAGAAACCTATTTCTGTAAGGTGATTTCAAGTGATGA 842
818 AAGATTAAAGACTATTTGTAAGAAATGCAATGAATGAAGTGAAGTGAAGTAAAGCA 877
843 ATTGAATGACATATAGCTGCTAATTTAGTGAACACTGATTTATGCTGCTAATCAAG 902
878 TGTATGACTCAAGTTCATCCAGAAATTTGTTCCAAAGGCAAAATTCATCAAGCAAG 937
903 TAGAGAGAGCCCAACATTTTAACTCCAGAAAGCAATGCAAGTGAAGAAAGAAAT 962
938 AAAACCCAAACGTGCTGTGCTCCACTGAGAGTGCAGTGAATCTTCAATTAACATCT 997

963 AAGAGAAATGCTTTCACTGAGTGCATTGACAGAGAGCTGCTCAATTAATTTA 1022
998 CAAGAGGAAATCTTGCTTGAAGTGTGTTGTAAGAGCTTGCACATCCACAGTTGA 1057
1023 CTGGCAAAAGAAATGTAATGCTTCCAAAAAGGACAGTTTATGAATCTTGAGAA 1082
1058 TTGAAACAAATTTGCTGTGACTTAACAAAGGGAGAGAAACAAAGAAATTAAGGCA 1117
1083 AACCTTGACATTCATTCATTTTCAAGAGACAGACTCTGAAATTTCAATGATTAAGCAA 1142
1118 GACTTGAAGATGAGATGCTCTTACAGAGCAAAAGAAATTTCTGCTGACAGCCAG 1177
1143 AAATCATTTAGAGCCATCCACATATTCATTTCTGTTAGTTAAAGGCTCCATCTG 1202
1178 CAATTTCTTGGAAACAGCACTACAGATTTTCAAGTTTATGAGAAAGAGCTCTCGCTG 1237
1203 GATCAAGCCCTCAAAATCTTGTCTGCTCCAGAGAGAGATGGAGACTTGAATGAG 1262
1238 GACAAAGAGCTCAGAGTGTGTTATAGACACCGAAGCAATGACATTTGTTATGTA 1297
1263 AGCTAATGCAACCCCAACCAAGAAATTTAGCTGTTAACAATGAGTCCCAATGAAT 1322
1298 GCTGAAAGAGAGCTCAACCCACATCAATGAGAGATCAATGCTCCCAAGTTGACA 1357
1323 TGCCTGTATGACCCAGCAGAAATTAATGAGGATACATTTATTTTCAATGTTCA 1382
1358 TCATCATTTTG---CTGTGATGTTGCTTCCCGAGAAATCAAGTTTACCACTTCA 1414
1383 AGAAAGATCAATGATGATATCATGTCATTCCTCTTAATGAATTTATTTATCTGGC 1442
1415 ACCAATCATATGCTGTGTAACAGTGTGAAGCTCAATGTCCATGCAATCTATCTTGC 1474
1443 AAACCATTTGTAATGCTGCTGAGCCACCAAGATCTCACTCACTGCAACACACT 1502
1475 CAATCCATATTTATGATGTTGATGATGCTCCCTCATTTGATCAACCAAGATGAGAAA 1534
1503 CTACAGATCATTTGCAACAGGCTGCTTTATCTAGACTGTGCTTTTGGTCTCTCT 1562
1535 TTAAGCTAAGTGTGGTACAGTCTTTCTTATCATTTGAGATCTTTGCTTCACTGA 1594
1563 CCCAATCATGATGTTTAAAGAGCTAAAGAAAGTCTTCTCATGAAGATTTATGT 1622
1595 GGCAGTGTGTCTGAGAGAGTGAAGAAAGTGAACCCCTGAGGAGGAGGCTATCA 1654
1623 TTTACATGAATTTGAACTTTGGAATCAAGATCTCATGATCTTTAAAGAAATTC 1682
1655 TATCTATGAATGCAATTTGAGATCAACAGAACCAAGAAAGATGCTGGTCTTA 1714
1683 TGTGCCCCAAAGACAGTACAGAACTTAATCGTGTGTCAGAGAAATTAAGGAT 1742
1715 CTATGTTGGTGAAGAAATGCTATAGGAAAACTGACATCAAGCCAAATTTGATTTAG 1774
1743 GGCAGAAATGAATTTCACTTACAGCCGGAATTTGCAATTTGCAAAAGAGATGAT 1802
1775 AAATCTCAAAACTTGAAGTTCCTTGAAGATCTGTATCTCCCAATTTGATATCT 1834
1803 GTCCTTGAATGCAAGTGAACATGATCAACCTTATCCCTCACTGCTGCTGCTGAA 1862
1835 TGAATTTAATTTGAAAGCAATTTGATCACTCATTTGAAACAGAGTTGAAAGTGTCTG 1894
1863 GACAAACAGGAACTGCCAGTATGAAGGTTCACTGTTGAAGATCAATCTAGTGT 1922
1895 GATTAAGTGAAGAGCTTTGA-----AATTAATGACAGAAAGATGACAGAT 1945
1923 AGCTATGCTAGTACATGACATGACAGGAGCACTACACGTGTGTGCGCAACACACTG 1982
1946 AATTAATGAGTGAATTTGACATATCTTAATGTAATTTAGAGGACCAAGATTTTA 2005
1983 CAGGCTCTCCGACAGGCTGCTGAGGCTGTTGCTCTCACTCCACCTGAGCTCCGT 2042
2006 CTGCTGTTAGTCACTATGCTCTGAGACAGTGTGCGAT---TAACTCAAGTAACTGT 2062
2043 TTACAGATGCCAAATCTCTCTTTGACTTGAACATGACAGATCAATTTGACAAAGTGT 2102

D	b	2063	TC	TTG	ATG	TC	CG	AT	TC	CA	CC	GA	AA	AC	CT	TC	A	CT	TG	T	CA	AA	GA	CA	GA	AG	GT	2122								
O	y	2103	TC	AG	TC	TC	AT	GA	CC	CA	GG	CG	AT	GA	CA	CA	AT	AG	CC	CA	TT	CA	AA	AT	T	CA	T	GA	2162							
D	b	2123	TC	GG	TC	GA	CC	TG	GA	AG	CT	GA	CC	CA	CA	CA	GA	CA	AT	TT	AG	CG	AG	T	AT	T	GT	GA	2182							
O	y	2163	AT	AT	CA	AT	TC	GA	AT	GC	CA	AG	CG	CT	GT	GC	CA	CC	AA	CT	GA	AT	TT	T	CT	GA	C	2222								
D	b	2183	AT	TT	GA	AG	GA	AA	CA	AA	GA	AG	CC	CT	GA	AG	GG	GA	AC	TC	GA	CA	GA	GT	CA	GA	AA	2242								
O	y	2223	AC	AG	CC	CA	AG	CC	CA	CT	GA	AG	CT	CT	CA	CT	GA	AA	CT	AC	T	CT	CC	CG	GT	GA	TG	GC	2282							
D	b	2243	GA	AA	CC	CA	AG	T	AT	CT	TA	CC	T	T	GG	CT	CA	T	T	T	GT	GA	AT	CA	GT	TC	AG	GT	CA	T	AG	2302				
O	y	2283	AG	TA	GA	CA	GA	TT	GG	GA	AG	CT	TC	CA	GG	AG	CG	CT	GA	CA	GT	AT	TT	T	GA	CG	AA	GC	2342							
D	b	2303	CG	TA	GA	CG	AA	GA	GA	GA	AG	TC	AG	CG	CT	AG	CG	CA	GC	CA	T	AT	GA	AA	CA	CA	CC	2362								
O	y	2343	CT	CA	GA	AC	CA	GA	T	TA	AA	AA	CC	CA	CA	CG	CT	GT	GA	AG	GA	CT	GG	AT	CA	GA	CC	T	GA	T	AT	2402				
D	b	2363	AG	CA	GC	TC	CA	GA	T	GA	GA	AT	CC	CA	AA	CA	T	AA	GG	TT	CA	AG	CT	TC	CA	CC	CA	GA	AA	T	2422					
O	y	2403	GG	AG	AT	T	CA	GT	GA	AG	CC	CT	GA	AT	GG	TT	GG	AA	T	CA	T	GA	T	GG	CC	CA	GC	CT	TC	GA	CA	2462				
D	b	2423	GA	TT	T	TA	AA	GT	GG	AG	CC	CT	TT	GA	AT	TC	AT	GA	GA	CA	GA	T	GA	CA	AG	AT	GA	C	2482							
O	y	2463	AG	TT	AG	CT	GG	CG	CC	CA	AA	GA	T	GT	GA	T	GA	T	GA	CA	T	CT	GT	GT	T	GT	GG	CA	AA	T	GT	2522				
D	b	2483	AG	TA	GC	CT	GA	AA	GC	CA	GG	AG	CC	CC	CA	GT	GA	AG	GG	GA	GA	AA	CA	GT	CA	CA	AA	CC	2541							
O	y	2523	AT	CC	CA	AT	AT	T	GT	CT	CA	GA	GC	CA	GC	CA	CT	T	T	TC	CA	T	CT	GA	T	CA	AA	GT	CA	GC	2582					
D	b	2542	-	AC	CA	T	TT	GG	GG	AT	GA	T	GA	CG	CC	T	GT	CT	TA	T	GC	CC	CT	TA	T	GA	T	GT	CA	AG	CT	CA	GC	2599		
O	y	2583	CG	TA	GA	T	GA	CA	T	GG	GG	CT	T	T	GG	CC	CG	CA	GC	T	GA	T	CA	T	GA	GG	GA	CA	AT	TC	GA	GA	2642			
D	b	2600	T	A	T	CA	T	CA	T	CA	AT	CA	CT	GA	AT	CT	GG	GC	CT	GA	CC	T	CA	GT	CA	T	GA	CA	CT	CA	T	AT	TC	GA	GA	2659
O	y	2643	CC	TC	CC	CA	T	GG	T	GG	CT	CC	T	GG	GA	AG	TC	GT	GA	AT	T	GG	T	GA	CA	GA	T	CA	CT	TA	GC	CA	2702			
D	b	2660	CT	AT	CC	TA	T	CA	AG	TC	CA	AG	T	GA	TC	CA	AG	GG	GT	GA	CC	T	T	TA	AA	CA	GT	CA	TT	TA						

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Db      3140 TATTACATATACACATCCATCAAAAGCCGAGTGGCACTCTCAAACTGAAATGCAACTAC 3159
Oy      3180 TCGATATAGCTTTTATTTCATGCAAAACATCAGAGATATAGGAAGTCAATTAACGA 3239
Db      3200 CAACTCAAAATTCCTACTTGAGGCGTTGCACCTTCAGAGGCGTGTGAAAAACGATACGGA 3259
Oy      3240 GGAA 3243
Db      3260 GGAA 3263

RESULT 9
US-10-435-751-2
; Sequence 2, Application US/10435751
; Publication No. US20040053348A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Paris, Mary
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 282P193 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-20084.00
; CURRENT APPLICATION NUMBER: US/10/435,751
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7650
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (272)...(3946)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 320
; OTHER INFORMATION: SNP = C/T = v.9
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 668
; OTHER INFORMATION: SNP = C/T = v.10
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1178
; OTHER INFORMATION: SNP = A/G = v.11
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3484
; OTHER INFORMATION: SNP = C/T = v.12
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4615
; OTHER INFORMATION: SNP = G/A = v.13
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Pos.: 5078; SNP = C/T = v.15
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Pos.: 5530; SNP = T/A = v.16
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Pos.: 5812; SNP = C/T = v.17
; FEATURE:

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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6114; SNP = A/G = V.18
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6229; SNP = C/T = V.19
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6383; SNP = G/A = V.20
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6626; SNP = C/T = V.21
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6942; SNP = C/T = V.22
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 7085; SNP = C/T = V.23
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 2684; SNP = A/G = V.24
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 3705; SNP = T/C = V.25
OTHER INFORMATION: Pos.: 5768; SNP = T/C = V.26
OTHER INFORMATION: Pos.: 6125; SNP = C/T = V.27
OTHER INFORMATION: Though these SNP variants are shown separately,
OTHER INFORMATION: they can also occur in any combinations and in any
OTHER INFORMATION: of the transcript variants listed in Figures 2A -
US-10-435-751-2

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
Best Local Similarity 48.8%; Pred. No. 1.1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;
QY 243 ACAGCTCCCAACCATCAACCAAGTCTCCAAAGATTACATATTGACCTTCGGAGAA 302
DB 367 ACAGGTTCCAAATATTAATAAGTCAAAAGTCCAAAGTTCCTTCCTTCGATGATGA 426
QY 303 TATTTGATTCAGTGTGAAGCCAAAGGAAACGCCCCCAAGCTTTTCTGACCCGTAA 362
DB 427 TTTTCAATTTGAATGTGAAGCTAAAGAAATCCAGAACCAACATTTTCGTGACTAAGA 486
QY 363 TGGAGTCACTTTTGAATGATGAATAAAGCCTCTGTCACATGAACCTTCGACAGAAAC 422
DB 487 TGGCAACCTTTTATTTTCACTGACCATGGATTAATTCATGCAACATTCAGAA----- 541
QY 423 GCTCATTAATTAACATCATGAGCAAGGAAAGCTGAACCTTATGAAGAGTCTATCAGTG 482
DB 542 ----AACTTCAGATTCCAAAAGGAGGACATATCTCACTTTCAAGGAAATACCGCTG 597
QY 483 TACAGCAAGAAAGAAAGCGGAGCTCAAGTTCTTAATTAACATTTGTCGCCCATCCAG 542
DB 598 CTTTGTCTTAATAATCTGGGAATCGTATGTCAAGAAATAGAAATTAATAGTTCAAG 657
QY 543 ATCAACCATTTGTGACCAAGAAATCTTGAACCAATCACTTCAAAAGTGTATGCTTT 602
DB 658 TGTTCAAAATCTCCAAAAGAAAAATGACCTCTTGAAGTGAAGAGGAGATCCAAAT 717
QY 603 AGTACTTCCTTGAGAGCCCAATTTGATTAACCAACCTATATATTTTGGATGATGA 662
DB 718 TGTCTTCCCATGGAATCTTCCAAAGGCTCCCACTTTTACATTTATTTGATGATAT 777
QY 663 TTTCTTTCAAAAGCTTTCACAAAGTGAAGATTTTCAAGTTTTGAATGGGAGACCTTTA 722

DB 778 TGAATTAGAACATCGAACCAAGATGAAGATATATCAAGCCAAAGGAGATCTATA 837
QY 723 TTTTTCATGTCCTCCAGAGACACCCGGAGACTATATCTGTTATGCTAGATTTAA 782
DB 838 CTTGGCAAAACGTGGAGAAAGAGACGTCCGATATACATCTGTTCTTGTGCAATTTCC 897
QY 783 TCATCTCAAAACCATACAGCAAGCAACCTATTTTCTGTGAAGTGAATTTCAATGATGA 842
DB 898 AAGATTAAAGACTATTTGTACAGAAATATCCAAATGAACCTAACAGTTTAACACA 957
QY 843 ATTGAATGACATATAGCTGTATTTATGAGCACTGAGTTTATGATGCTAATTCAG 902
DB 958 TGTATATGACTCAATTTATCCAGAAATGTGTTCAAGGCAATTCATACCAAAAG 1017
QY 903 TAGAGAGAGCCCAACATTTTAACTCCAGAAAGCAATGCAATGAACAAAGAAAT 962
DB 1018 AAAACCCAACTGCTGTGCTCCCACTGAGAGTGGCATGTGTTCAATTACATCCT 1077
QY 963 AAGAGAAATGTCTTTCACTGAGTGCATTCAGAGAAAGTCTTACCCCAATTTATTA 1022
DB 1078 CAAGGGGAAATCTTGCTGTGATGTTTGTGAAGGCTTGCCCACTCCACAGTTGA 1137
QY 1023 CTGGCAAAAGAAATGGAATGCTACCAAAACAGCAAGTTTAAGAACTTTGAGAA 1082
DB 1138 TTGGAACAAATTTGTGTGATCTTACAAAGGGGAGAAACAAAGAAATTTATGCAA 1197
QY 1083 AACCTTGACATCATTCATGTTTCAAGACAGACTCTGAAATTTCAATGATATGCAAA 1142
DB 1198 GACTTTGAAGATGAGAAATGTCTCTTACAGAGCAAAAGAAATTTCCCTGACAGCCAG 1257
QY 1143 AAATCATTTAGAGCCATTCACATCAATTCATTTCTGTGAAGTTAAAGCGCTCCACTG 1202
DB 1258 CAATTTCTTGGAAACAGCACTCAAGATTTTCAAGTTATGAGAAAGACCTCCGCTG 1317
QY 1203 GATCAGACCCCTCAAAATTTGTGCTGTGCTCCAGAGAGATGGGACCTTGAATGTCAG 1262
DB 1318 GACAAAGAGCTCTGAGTGTGTATGACACCGAAAGCAATGSCATCTGTATATGGA 1377
QY 1263 AGCTAATGCAACCCCAACCCAGATTAAGTGTAAACAAATGAGTCCCAATGAAT 1322
DB 1378 GGTGAGAGAGAACTTCAACCAATCAATGAGAGATGATGCTCCCAAGTTGACAA 1437
QY 1323 TGCCCTGATGACCCCAAGCAAAATGAGTGGATACCATTTTTCATTAATGTTCA 1382
DB 1438 TCATCATTTG---CTGTGATGTGTCTTCCCAAGGAAATCACTTTTACCACTTCA 1494
QY 1383 AGAAATGATCAAGTGAATATCAAGTGAAGTCCCTAATGAATATGATATTTACTGGC 1442
DB 1495 ACCAATCATACTGCTGTGTACAGTGTGAAGCTTCAAAATGTCATGGAATATCTTGGC 1554
QY 1443 AAACCATTTGAAATGTGCTGCTGAGCACACGAATCTTCAACCTGCAACACACT 1502
DB 1555 CAATGCCAATATTTGATGTTGTGATGTCCGTTCATGATCAACCAAGATGAGAAAA 1614
QY 1503 CTACAGGTCATTTGAAACAGGCTGTTTACTAGACTGTGCTTTTGGTCTCTCT 1562
DB 1615 TTAAGCTACAGTGTGGGTGATGATGCTTTTCAATTTGCGAGTTCTTTGCTTCACTGA 1674
QY 1563 CCCAACATCGAGTGTTTAAAGAGCTTAAAGAAAGTGTCTTCAATGAAGATTTATGCT 1622
DB 1675 GGCAGTGTGTCTGCGAAGAGTGAAGAAATGAAACCCCTGAGAGGCGAGGATATCA 1734
QY 1623 TTTTACATGAATATGAACTTTGGAATCAAAATGCTCATATGATGCTTTTAAAGAAATCC 1682
DB 1735 TATCTATGAATATGGAATCTTCAATCAACGAACCAAGAAAGATGCTGGGTCTTA 1794
QY 1683 TGTGGCCCAAAAGACATGACAGAACTTATATCGTGTGTGCAAGAAATTAATTAAGGAT 1742
DB 1795 CTATGTTGGATGAAGAAATGCTATGAGAAATCTCAAGTCAAGCAATTTGATATAG 1854
QY 1743 GGCAAAGATGAATTCATCTTACAGCCGGAATATGCAATGTGTGCAAGAGAGATGCT 1802
DB 1855 AAATGCTACAAATTAAGATTTCTTAAAGATCTGTATCTCCCAATTTGCAATGTCT 1914

QY 1803 GTTCCTTGAATGCAAGTGAACATGATCACACCTTATCCCTCAGTGTCTGTGGCGAA 1862
 DB 1915 TGAATTAACATTTGGAAGAGAAATGTGACTACATTTGAAACACAGTTTGAAGTTGCTG 1974
 QY 1863 GGAACAACAGGGAATCTGCCAGTGAATGAAGGTTCACTGTTGACAAAGATCATCTAGTGT 1922
 DB 1975 GAGTAAGAATGAGAAAGCCCTTTGA-----AATTAAATGGCAGAAATGGCAGAGAT 2025
 QY 1923 AGCTGATGTCAGATGAGATGACAGCGGAGCCTACAGTGTGTGCCCAACACCACTCTGCA 1982
 DB 2026 AATTATTAATGAGGCTTAATTTGACATATCTAATGTAATCTTAAGAGACCAAGATATTTA 2085
 QY 1983 CAGCGCTCCGCGCAGGCGCTGTGCTTACGCTTGTGCTCTACTCTCAACTCCAGCTCCGCT 2042
 DB 2086 CTGCTTTGAGCTCATCTGCTCTAGACAGTGTGCTGCCGAT---TAACTCAATTAATCTGT 2142
 QY 2043 TTACGATGTCCCAATCTCTCTTTGAATTGAATGACAGATCAACTTGAACAAAGTGT 2102
 DB 2143 TCTTGAATGTCCGGAATCCACAGAAACCTTCACTGTCTGAAGAAGACAGAAACAGAGTGT 2202
 QY 2103 TCAGCTGTATGGAACCCGAGCGATGACAAACATTAAGCCCATTAACAAATTCATCTCA 2162
 DB 2203 TCGGCTGACCTGGAAAGCTGAGAGCTACCAACAGCAATATTAGCAGATATATTGTGA 2262
 QY 2163 ATATGAAGATGCAATGACACAGCCAGGCGTGTGGACACACCAACTGAAGTTTCTGGAAC 2222
 DB 2263 AATTGAAGAGAAACAAAGAGAGGCTGGAAGTGGAGAACTGACAGAGTCCAAAGGAA 2322
 QY 2223 ACAGACCAACGCCAGCTGAAGCTGTCTCTTAAGTAACTACTCTTCCGCGTGAATGC 2282
 DB 2323 GAAACACAGATATCTTACCTTGGCTCCATTGTAAGATACAGTTCAGGCTCATATAG 2382
 QY 2283 AGTGAACACATTTGGGAAGAGCTTGGCCAGCGAGGCTCTGAGCAGTATTTGACGAAGC 2342
 DB 2383 CGTGAACGAGTAGGAGAGAGTCAAGCTTACCGCGCTGACAGCAATCATGAAACACACACC 2442
 QY 2343 CTCAGAACGAGATTAATAACCCCAAGCTGTGGAAGAGCTGGATCAGAGCTGATATTT 2402
 DB 2443 AGCAGCTCCAGATGAGATTCACAAACATTAAGGTTCAAGCTCTCCAAACCAAGGAAT 2502
 QY 2403 GGAGATTAACGTGGAAGCCCTTGAATGTTCGATTAATGAGGCCAGGCTTCAGTACA 2462
 DB 2503 GATTAATAAGTGGAGACCTTTGAAATCATGAGCAGAAATGAGCCAGGCTTGAAGTACAG 2562
 QY 2463 AGTTAGCTGGCCGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2522
 DB 2563 AGTGAACCTGGAAGCCACAGGAGGCCCAAGTGGAGTGGAGAAAGAAACAGTCAACAAAC- 2621
 QY 2523 ATCCAAATATATTTGTCTCAGGACGCCCACTTTGTTCCATACCTGATCAAAAGTTAGGC 2582
 DB 2622 --ACACATTTGGCGGTATGATACGCTGCTCTATGCTCCCTTATGATGATCAAGCTCCAGGC 2679
 QY 2583 CCTGAATGACATGGGGTTTCCCGCCGAGCAGCTGATGATGATGATGATGATGATGATGATG 2642
 DB 2680 TATCAATCACTAGAGATCTGGGCTTGAACCTGACAGTCAAGTCACTCTATTTCTGAGAGAGA 2739
 QY 2643 CCTCCCAATGTGTGCTCTGAGGAAAGTGTGATGATGATGATGATGATGATGATGATGATG 2702
 DB 2740 CTATCTGTATGACGCTCCAGTATCATGAGGGTGGAGCTTATTAACAGTACATTAAGTTTAA 2799
 QY 2703 GGTGACCTGGAGCCGATCCTCTGAAAAGCATCCGAGGACCTTACAGAGGCTATGAGAT 2762
 DB 2800 AGTTACTTGTGTAACAGTTCTCAAGAGACAGATGACATGAGACGCTGAAAGGCTATAGAT 2859
 QY 2763 TTACTATTTGAAAGACCCAGAGTTTCACTTAAAGAAACAGAGCTCACTTGAAGAAAGAT 2822
 DB 2860 AATATTTGTGAAACCAAAAGTCTGTGATGGAAGAAACACATCCCAAGAGTGAACAT 2919
 QY 2823 CCTCACTTCCAGAGGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2882
 DB 2920 TCTAAGATTTTCAGGACAAAGAACTGTGAATGTTCTTCTCTTGAATGATGATGATGATGATG 2979

QY 2883 CTACACACTGAATGTCCGAGTGTGATGATGGAAGGGGAGGGCCAGCCAGCTTGACAG 2942
 DB 2980 AATTCAATTAACAGTCTTAAAGCTTAACTTAATGAGAGCTGGTCTGAAAGTGAAGCTTA 3039
 QY 2943 AGCTTTAATTAATCTCCAGAAAGAGTCCCAAGTGTCTCTGCTTTGAAGATGTGATTC 3002
 DB 3040 TATATTTCAAAACCAAGGAGGATGCTGAAACAGCCACTTTTCTAAGGTCAATCAAGT 3099
 QY 3003 AACACTGACCTCTCACTTTGGAATGGATGCAACGAGCCACCGGAATGGCAATTTGAC 3062
 DB 3100 TGATTAAGACACTGCGCACTTATCTTTGGGACTTACTTAAGAAATTAATGAAACTTAAC 3159
 QY 3063 AGAGTACACCTTAAAGTATCAGCAATTAACAGCAGATGATTAAGCCCTCTGTGATA 3122
 DB 3160 TGGCTATCTTTTGCATATACATTAATTAATGACACCTGAGATTTGAGAAATTAATGA 3219
 QY 3123 TTTGAAATTT---CCTGCCAAGACACGCTGACTTTAAATAATTTAATTTAGCAC 3179
 DB 3220 TATTAACATTAACACTCCATCAAGCCGCTGGGACCTTCAAACTGAATGCAACTAC 3279
 QY 3180 TCGATTAAGTTTATTTCTATGACAAACATCAGAGGATGAGAAAGTCAATTAACA 3239
 DB 3280 CAGTACAAATTTCTTCTGAGGCTTGACCTTCAAGGCTGTGAAACCAATCAGCA 3339
 QY 3240 GGAA 3243
 DB 3340 GGAA 3343

RESULT 10
 US-10-435-751-152
 ; Sequence 152, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Ralciano, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT APPLICATION NUMBER: US/10/435,751
 ; PRIORITY FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; PRIOR FILING DATE: 2002-11-01
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 7650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-435-751-152

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
 Best Local Similarity 48.8%; Pred. No. 1.1e-127;
 Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

QY 243 ACAGCTCCACCAACCAACCCACCAAGCTCTCCAAAGATTAATTAAGACCTCGGGAGAA 302
 DB 367 ACAGGTTCCACCAACCAACCAACCAAGCTCTCCAAAGATTAATTAAGACCTCGGGAGAA 426
 QY 303 TATTTAATTCAGTGTGAGGCAAGGAAACCGCCCAAGCTTTTCTGAGACCCGTAA 362
 DB 427 TTTTAAATTTGAATGTGAAGCTTAAGGAAATTCAGAACCAATTTTGTGAGCTTAAGA 486
 QY 363 TGGAGCTATTTTGAATGATTAAGACCTCTGTGATCAACATGAAGCTTGACAGGAAC 422
 DB 487 TGGCAACCTTTTATTTTCACTGACCAATCGGATTAATTCATGAACCAATTCAGAG- 541

OY	423	GCTCAATTAATTAACATCATGAGCGAAAGGAAAAGCTGAGACTTAATGAGAGATCTAATCAAGT	482
Db	542	-----ACATTCCAGAGATCCCAAAACGAGGGGCAATATCTCACTTTCAAGGGAATACCCGTG	597
OY	483	TACAGCAAGAAACGAACCGGAGCTGCAAGTTTCTTAATTAACATTTGTGCCGCATCCAG	542
Db	598	CTTTGCTTCAATTAATTAATCTGGGAATGCTATGTGCAGAGAAATTAATTAATTAATGTTCCAG	657
OY	543	ATCAACATTTGTGAGCAAAAGAAAACTTGAACCAATCACTTCAGAGTGCATCTTT	602
Db	658	TGTTCCAAAACCTCCAAAAGAAAAATTGACCCCTTGAATGTGAGGAGGAGATCCAAAT	717
OY	603	AGTACTTCCCTGCGAAGCCCCCAATTTGATTAACACACCTTAATTAATTTTGGATGATTA	662
Db	718	TGTCTCTCCATGCAATCCTCCCAAGGCGTCCACCTTTACACATTAATTTGGAATAT	777
OY	663	TTCCCTTCAAAAGACTTCCAAAAGTGAAGAGTTCTCAAGTTTGAATGGGACCTTTA	722
Db	778	TGAATTAAGAACATCGAACAAGATGAAGATATACATGAGCCAAAAGGAGATCTATA	837
OY	723	TTTTTCCAAATGTCCTCCGAGAGACACCCGGAGACTATATCTGTAATGCTAATTTAA	782
Db	838	CTTGCGAAACGAGGAAAAAGGACAGTCGCAATGATCACTAGTCTTGTGCTGATTTCC	897
OY	783	TCATATCTAAACCATACAGCAGAGAACACTATTTTCTGTGAAGTGAATTCAGTGAATGA	842
Db	898	AAGATTAAAGACTAATTTGTACAGAAATGCCATGAACTAAACAGTTTAACGTTTAAAGCA	957
OY	843	ATTGAATGACACTAAGCTGCTAATTTAGTGAAGCACTGATTTTAATGCTGAATCAAG	902
Db	958	TGCTAATGACTCAATTCATCAACAGAAATTTGTTCCAAAGCAATTCATACAGCAAG	1017
OY	903	TAGAGAGAGCGCACCAACATTTTAACTCCAGAAAGCAATGCAATGAACAAAGAGAAAT	962
Db	1018	AAAAACCAAACTGCTGTTGCTCCCACTGAGAGTGCAGTGAATCTCAATTAACATCCT	1077
OY	963	AAGAGAAATGTGCTTTCACTGAGATGATTCGAGAGAGACTGCTTACCCCAATTAATTTA	1022
Db	1078	CAAAAGGGGAAATCTTGCTGCTTGAATGTTTGTCTGAAGCTTGGCCAACTCCACAGGTTGA	1137
OY	1023	CTGGGCAAGGAAGATGGAATGCTAACCCAAAACAGGACAGTTTAATGAACCTTTGAGAA	1082
Db	1138	TTGGAAACAAATTTGTGTGACTTACCAAAAGGGAGAGAAACAAAGAAATTAATGGCA	1197
OY	1083	AACCTTGAGATCATTTCAATGTTTTCAGAGACAGACTCTGGAATTAACCAATGTATAGCAA	1142
Db	1198	GACTTTGAAGATAGAGATGTGCTCTACAGAGACAAAGAAATTAATGCTGCAAGCGAC	1257
OY	1143	AAATGCAATTAGAGACCATCCACCATCACTTTCTGTTAGATTAAGCGGCTCCATACTG	1202
Db	1258	CAATTTCTTGGGAAACGGCACTACAGATTTTCACTTTATAGTAGAAGAGCTCTCTCGGTG	1317
OY	1203	GATCAACGCCCTCAAAATCTTTGTCGTGCTCCGAGAGAGGTGGGACTTGATCTGCAAG	1262
Db	1318	GACAAAGAGCTCAAGAGCTGTGTATAGCACCGGAGCAATGGCACTTGTATGTGA	1377
OY	1263	AGCTAATGGCAACCCCAAAACCCAGATTAAGCTGTTTAACAATGGAGTCCCAATAGAAT	1322
Db	1378	GGCTGAAGAGAACTCAACCCACATCAAGTGAAGATCAATGCTGCCCAAGTTGACAA	1437
OY	1323	TGCCCCGTATGACCCCGACAGAAAAATAGATGGCAGTACCAATATTTTTCAAATGTTCA	1382
Db	1438	TCATCCATTTG---CTGGGATGTTGTCTTCCCGAGGAAATCAGTTTTCACCACTTCA	1494
OY	1383	AGAAAGATCAAGTGCAGTATATCAAGTGCATATGCCCTTAATGAATTTGATATTAATCTGGC	1442
Db	1495	ACCAATCAATCTGCTGTGTACAGATGGAACCTCAATATGCCATGGAACCTATCTTTGC	1554
OY	1443	AAAGCATTTGTTAAATGTGCTGGCTGAGCAACGAATTCCTCAACCTCGAAACACACT	1502
Db	1555	CAATGCCAATATTAATGTTGTGTGATGTCCGTCACTTAATGAACAAAGATGAGAGAAA	1614
OY	1503	CTACAGGTCATTTGCAAAACGAGCTGTTTACTAGACTGTGCTTCTTTGGGCTCTCT	1562

Dd	1615	TTAGCGTACAGTGGTTGGGTACAGTGGCTTTCTTACATTTGGGAGTTCTTTGGCTTCACTGA	1674
Qy	1563	CCCAACCATCGAGTGTGTTTAAAGAGCTAAAGAGTGTCTTTCATGAAATATTAATG	1622
Dd	1675	GGCAGTGTGTGCTCGCAGAAAGGTGAAGAAAGTAAACCCCTGAGAGGCGAGCGATATCA	1734
Qy	1623	TTTTCATGAAATATGAACTTTGGAAATCAAAAGATGCTACATGGAATCGTTAAAGAAATTC	1682
Dd	1735	TATCTATGAAATATGGCATTGGCAGATTCACAGAACACAGGAAGAAATCTGGGCTTCA	1794
Qy	1683	TGTGGCCCAAAAGSACGATCAGGAATTATACGTGTGTGCAAGGAATTAATTAGGAT	1742
Dd	1795	CTCATGTTGGGTAGAAAATGCTATAGAAAACTGCAGTCAACGCCAATTTGGATATAG	1854
Qy	1743	GGCAAGAATGAAATTCATTACGACCCGAATATGCAAGTTGTCAAAAGAGGAGCATGT	1802
Dd	1855	AAATGCTACAAAATTAGAGTTTCTCTAAGAAATCCTCGATCCCAAAATTGCAATATGCT	1914
Qy	1803	GTCCTTGAATGCAAGTGAACATGATCACCCTTATCCCTCACTGTCTGTGGCTGAA	1862
Dd	1915	TGAATTACATTTGTGAAAGCAAAATGTGCTCAATTTGAAACACAGTTTGAAGTTGCTTG	1974
Qy	1863	GGACAACAGGGAATGCGCCAGTATGAAAGTTCACTGTTGACAAAGGATCATATAGGT	1922
Dd	1975	GAGTAAAGATGGAAGACCTTTGA-----AATTAAATGGCACGAAGATGGCAGAT	2025
Qy	1923	AGCTGATGTCAGTGACATGACAGCGGGAACCTACACGTGTGGCCAAACAACACTGGA	1982
Dd	2026	AATTATTTATGATGAGCTAATTGACCAATATCTAATGTAACTTTAGAGGACCAAGTATTTA	2085
Qy	1983	CAGCGTCTCGGCACGCCGTGTGTTAGCGTTGTGCTCTTACTTCAACTCAGCTCCCGT	2042
Dd	2086	CTGCTGTTCAAGCTCATCTGCTCTAGACAGTGGCTGCCGATA---TAACTCAAGTAACTGT	2142
Qy	2043	TTAGAGTGTCCCAATCTCCCTTTGACTTAGAATGACAGATCAACTTGACAAAAGTGT	2102
Dd	2143	TC TTGATGTTCCGATCCACAGAAAACCTTCACTTGTCTGAAAGACAGAACAGAGTGT	2202
Qy	2103	TCAGCTGTCAATGACCCCGAGCGATGCAACAATAGCCCAATTACAAATTCATCATGCA	2162
Dd	2203	TCGGCTGACCTGGGAACGTGAGCTGACCAACAAGCAATTTAGCGATATTTGTGTA	2262
Qy	2163	ATATGAAGATGCAATGCAACAAGCCAGGGCTGTGGCACACCAAACTGAAGTTTCTGAAAC	2222
Dd	2263	ATTTGAAGGAAACAAAGAGAGCTCTGGAAGTGGAGAACTGACAGAGTCCAAAGGAAA	2322
Qy	2223	ACACAACAAGCCAGCGTGAAGCTGTCTCTTACGTGAATCAATCCCTTCGCGGATAGG	2282
Dd	2323	GAAAACCAAGTTATCTTACCTTTGGCTCCATTTGTGATACCAAGTTCAGGGTCATAGC	2382
Qy	2283	AGTGAACGCAATTTGGGAAGAGCTTGGCCAGCGAGGCGCTGAGCAGTATTTGACGAAGC	2342
Dd	2383	CGTGAACGAATAGGAGGAAGTACGCTTACGACGCCGTCAAGACATATGAAACACCAAC	2442
Qy	2343	CTCAGAAACCAATTAATAAACCCCAAGCTGTGGAAGGACTGGGATCAGAGCTGTGTAATTT	2402
Dd	2443	AGCAGCTCCAGATGAGAAATCCACAAAACATTAAGGGTTCAAGGCTTCAACCCCAAGAAAT	2502
Qy	2403	GGAATTAACGTGGAAGCCCTTGAATGTTTCGAATCTAATGGGCAAGGCTTTCAGTACAA	2462
Dd	2503	GATTATTAAGTGGAGGCTTTGAAATCCATGTGAGACAGAAATGGAACAGGCTTGAAGTACAG	2562
Qy	2463	AGTTAGCTGGGCGCAGAAAGATGATGTATGATGATGACATCTGTGGTTGTGCAAAATGT	2522
Dd	2563	AGTGAACCTGGAAGCCACAGGAGGCCCAATGTGAGTGGAGGAAGAAACAAATCACAACCC-	2621
Qy	2523	ATCCAAATATATTGTCTCAAGCACGCCAACCTTTGTTCCATACCTGATCAAAAGTTCAGC	2582
Dd	2622	--ACACATTTGGGGTATGACGCTGTGTCATAGCCCTTATGATGTCAAGGTCACAGGC	2679
Qy	2583	CTGGAATGACATGGGGTTTGCCCCGACCAAGCTGTATGTATGGGAATTTCTGGAGAGA	2642

Db 2680 TATCATCACTAGAGTCTGAGCTGAGCCCTGAGTCAGTCACTCTATTTCTGAGAGAGA 2739
 QY 2643 CCTCCCAATGAGTGGCTCTGGGAAGCGTGGTGAATGTGGAACAGTACCTTAGCCGA 2702
 Db 2740 CTATCTGTATACAGCTCCAGTGTATCATGAGGAGCGTTATTAACAGTACATTAGTTAA 2799
 QY 2703 GGTGCACTGGAGCCAGTACTCTGAAAAAGCATCCGAGGACACTTAAGAGGCTATCGAT 2762
 Db 2800 AGTACTCTGTGCAAGCTTCCAAAGGACAGAGTACATGACGCTGAAAGGCTATCAGAT 2859
 QY 2763 TTAATCTTGAAGAGCCAGAGTCTTAATAAGAAACAGACGTCACATTGAGAAAAAGAT 2822
 Db 2860 AATATGTTGAAAAACAAAAAGTCTGTGATGGAAGAACACATCCAAAGAAAGTGAACAT 2919
 QY 2823 CCTCACTCTCCAGGAGAGACATCTAGTCAATGTCAGGCTGAGCCCTGAGCCCTTAGCCA 2882
 Db 2920 TCTAAGATTTTCAGGACAAAGAACTCTGAAATGTTCTTCTTGAATGAGCTTAAAGTA 2979
 QY 2883 CTACACACTGAATGTCCAGTGGTCAATGGGAAGGAGGAGCCGAGCCGCTGACAG 2942
 Db 2980 ATTTCATTAAAGCTTTAGCCATTAATCTTAAGAGAGCTGTGCTGAAAGTGAAGCTTA 3039
 QY 2943 AGCTTTTAATCTCCAGAAAGAGTCCCAAGTGTCTCTGCTTGAAGATGTGAATCC 3002
 Db 3040 TATATTTCAAAACACGAAAGAGTACTGAACAGCAACTTTTCTAAAGTCACTAAAGT 3099
 QY 3003 AACACGTGACTCTCTCACTTTGGAATGGATCCAGGAGCCACCCGAATGGCATTTTGA 3062
 Db 3100 TGATTAAGACACTGCGACCTTTATCTTGGGACTACTTAAGAAATTAAGAAACTTAAC 3159
 QY 3063 AGAGTACACCTTAAGATATCAGCAATTAACAGACACATGAATTAAGCCCTCTGTGATA 3122
 Db 3160 TGGCTATCTTTGCAATATCAGATTAATTAATGACACTGAGATTTGAGAAATTAATGA 3219
 QY 3123 TTTGAAATTT---CCTGCCAACAAGACACGCTGACTTTAAAAATTTAAATTTGACAC 3179
 Db 3220 TATTAACATTACAACTCCATCAAGGCCAGCTGACCTCTCAAACTGAAATGCACTAC 3279
 QY 3180 TCGATTAAGTTTATTTCTATGACAAACATCAGAGATCAGAAAGTCAATTAACAA 3239
 Db 3280 CAAGTACAAATTTCTACTTGAAGGCTTGCACTTCAAGGGCTGTGAAAAACGATACGGA 3339
 QY 3240 GGAA 3243
 Db 3340 GGAA 3343
 RESULT 11
 US-10-435-751-158
 ; Sequence 158, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Faries, Mary
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT APPLICATION NUMBER: US/10/435,751
 ; PRIOR FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; PRIOR FILING DATE: 2002-11-01
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 158
 ; LENGTH: 7650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-435-751-158
 Query Match 11.4%; Score 469.6; DB 13; Length 7650;
 Best Local Similarity 48.8%; Pred. No. 1.1e-127;
 Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;
 QY 243 ACAGCTCCCAACCATACACCAACAGTCTCCAAAGATTACATTATGACCTCGGAGAA 302
 Db 367 ACAGGTTCCAAACATTAATAAACAGTCAAAAGTCCAAAGTGGCTTTCCCTTGATGAGTA 426
 QY 303 TATTTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTCTGAGCCGTAA 362
 Db 427 TTTTCAAAATGATGTGAAGCTTAAGAAATCCAGAACCAATTTTGTGTGATAGGA 486
 QY 363 TGGGACTAATTTGATCAATGAATGAAGCCCTGTGTCACATGAAGCCGACAGGAAC 422
 Db 487 TGGCAACCTTTTATTTTCACTGACCATGGAATTAATCCATGAAACATTCAGA----- 541
 QY 423 GCTCAATTAATTAACATCATGAGGAGAAAGCTGAGACTATGAGAGAGTCTATCAGTG 482
 Db 542 ----ACATTAGAGATCCGAACGAGGGGCAATATCTCACTTTCAAGGAAATACCGCTG 597
 QY 483 TACAGCAAGAAACGAACGCGAGCTGCAAGTTCTAATAACATTTGTTCGCCCATCCAG 542
 Db 598 CTTTGCTTCAATTAATCTGGGAATGCTATGTCAAGAAATTAAGAAATTAATTAATTA 657
 QY 543 ATCAGCATTTGTGAGCAAGAAAGAACTGAACCATCACTCAACTGAAGTGTCAAGTCTTT 602
 Db 658 TGTTCCTCAAACTCCCAAGAAAGAAATTAAGCTCTTGAAGTGGAGAGGAGATCCAT 717
 QY 603 AGTACTCTCCGACAGACCCCAATTGATTAACACCACTTAATATATTTTGGATGATTA 662
 Db 718 TGTCTCCCATGAGATCTCTCCCAAGGCTCCCACTTTTACACATTTATGATGAATAT 777
 QY 663 TTTCTTTCAAGACTTCCAAAGTGAAGATTTCTCAAGTTTGAATGGGACCTTTA 722
 Db 778 TGAATTAAGAACATCAAGAAAGAAAGTATATATGATGAGCCAAAGGAGATCTATA 837
 QY 723 TTTTTCATATGCTCTCCAGAGAGACCCGGAAGACATATCTTTATGCTAGATTTAA 782
 Db 838 CTTTCCAAACGTGGAAGAAAGAGACATGCAATGACTGCTTGTCTTGTGCAATTTCC 897
 QY 783 TCATACCTCAACCATACAGACAGAAAGCACTAATTTCTGGAAGTGTATTCAGTGAATGA 842
 Db 898 AAGATTAAGACATATTTGACAGAAATGCAATGAACTTAACAGTTAAAGTAAGCA 957
 QY 843 ATTGAATGACATATAGCTGCTAATTTGATGACACTGAGTTTATGTGCTAAATCAAG 902
 Db 958 TGTCTAATGACTCAAGTTCATCAAGAAATTTGTTTCAAGGCAATTCATCAACCAAG 1017
 QY 903 TTAGAGAGGCCCAACATTTTAACTCCAGAAAGGCAATGCAAGTAAACAAAGAGAAAT 962
 Db 1018 AAAACCTCAACCTGCTGTGCTCCCACTGAGAGTGGCAGTGAATCTTAATTAACATCT 1077
 QY 963 AAGAGAAATGCTTTCATCTGAGTGAATGCAAGAGAGCTCTTACCCCAATTAATTTA 1022
 Db 1078 CAAGGGAAATCTTGTCTGTGATGATGTTTGTCTGAAGGCTTCCCACTCCACAGTTGA 1137
 QY 1023 CTGGCAAGAGAGATGAAATGCTAACCAAAACAGACAGTTTAAAGAACTTTGAGAA 1082
 Db 1138 TTGAAACAAATTTGTGTGACTTCAACAAAGGGAGAGAAACAAAGAAATTAATGAGCA 1197
 QY 1083 AACCTTGACATCTATCTGTTTTCAGAGAGAGCTCTGGAATTAACAAATGATAGCAAA 1142
 Db 1198 GACTTTGAAGATGAGATGTCTCTTACAGAGACAAAGAAATTAATGCTGACAGCCAG 1257
 QY 1143 AAATCATTTAGAGCATCCACCATATCATTTTGTGTGATTAAGAGGCTCTCATACTG 1202
 Db 1258 CAATTTCTTGGAGACAGCACTACAGATTTTACAGTTTATATGAAAGGCTCTCCGCTG 1317
 QY 1203 GATCAACGCCCTCAAAATCTTGTGCTGTCTCCAGAGAGAGATGGAAGCTTGTATCTGAG 1262
 Db 1318 GACAAAGAGCTCTGAGTGTGTATGATAGACCGAAGACATGGAATCTTGTATGTA 1377

QY 1263 AGCTAATGGCAACCCCAACCCGAGATTAAGTGTGAACAATGAGAGTCCCAATAGAAAT 1322
 DB 1378 GGTGAGAGAGAACTCAACCCCAATCAAGTGAAGATCATGCTCCCACTGACAA 1437
 QY 1323 TGCCTGATGACCCGAGAGAAAATAGATGGCGATACCATTAATTTTTCAAATGTTCA 1382
 DB 1438 TCATCATTTG---CTGGATGATGTTCTTCCCAAGGAAATCAGTTTACCAACTTCA 1494
 QY 1383 AGAAGATCAAGTGCATATATCAATGCAATGCTCTTAATGAATATGATATTTACTGCG 1442
 DB 1495 ACCAAATCACTACGCTGTGTACAGTGAAGCTAAATGTCATGAGAACTATCTTTC 1554
 QY 1443 AAACGATTTGTAATGCTGCTGAGCAACCAAGATCTTCACTCAACCTGAAACACT 1502
 DB 1555 CATGCAATATATGATGTTGTGATGCTCGTCCATGATTAACAACCAAGATGAGAAA 1614
 QY 1503 CTACAGGTCATTTGCAACAGGCTGCTTAACTAGACTGCTTCTTGGGTCTCTCT 1562
 DB 1615 TTACGCTACAGTGTGGGTACAGTCTTCTTACATGCGAGTTCTTGGCTTCACTGA 1674
 QY 1563 CCCACATCGAGTGTTTAAAGAGACTAAAGAAATGCTCTTCAATGAATATTTATGT 1622
 DB 1675 GCGAGTGTCTCTGAGAGAGTGAAGAGAAACCCCTGAGAGGAGCGGCTATCA 1734
 QY 1623 TTTAATGAAAATGAACTTTGGAATCAAGATGCTACATGGATGTTAAAGAAATTC 1682
 DB 1735 TATCTATGAAAATGCACTGTCAGATCAACAGAACCAAGAGATGCTGGCTTA 1794
 QY 1683 TGTGCCCCAAAGAGACATACAGAACTTATACGTGTGTCAGAGAAATTAATGAGAT 1742
 DB 1795 CTATGTTGGGTGTAATAATGCTATAGAAAACCTGAGTCAACAGCAATTTGGATTAAG 1854
 QY 1743 GCGAAAGATGAAATCACTTACAGCCCAATAGAGTTGTCAGAAAGGAGAGATGAT 1802
 DB 1855 AAATGCTCAAAAATTAGATTTCTCTAAGAAATCTCGATCCCAATTTGCAATGCT 1914
 QY 1803 GTCTTTGAATGCAAGTGAACATGATCAACCTTATCCCTCACTGCTGCTGCTGA 1862
 DB 1915 TGAATTAATGTAAGAAAGCAATGTGATCACTTTGAAACAGATTTGAATGTCG 1974
 QY 1863 GGAACAACAGGAACTGCCAGTATGAAGTTCACTGTTGACAGAGATCACTAGTGT 1922
 DB 1975 GAGTAAGATGAGAGACCTTTGA-----AATTAATGCGACAGAAATGCGAGAT 2025
 QY 1923 AGTGAATGTCAGTGAAGATGACAGCGGAGCTACAGTGTGTGCCAACACACTGTGA 1982
 DB 2026 AATTATTTGATGAGCTAATTTGACATATCTAATGTAATCTTAAAGAGACCAAGTATTTA 2085
 QY 1983 CAGCGTCTCCGAGCGCTGTGCTTACGCTTGTGCTCTCACTCAACTCCAGCTCCGT 2042
 DB 2086 CTGCTGTGAGCTCATCTGCTCTTACAGCTGTGCGATTA---TAACTCAATCACTGT 2142
 QY 2043 TTACAGATGCTCAATCTCTCTTTGACTTAAGATGACAGATCAACTTGAACAAAGTGT 2102
 DB 2143 TCTTATGTTTCCGAGATCAACAGAAACCTTCACTTGTGAAAGACAGAAACGAGTGT 2202
 QY 2103 TCGCTGTATGAGACCCGAGGAGTGAACAACATATGAGCCCATTAACAAATTCATCTCA 2162
 DB 2203 TCGGCTGACCTGGAGAGTGAAGTGAACAACAACATATTTAGGAGATATTTGTGA 2262
 QY 2163 ATATGAAGATGCAATGCAACAGCGAGGCTGTGCAACCAACATGAAGTTTCTGAAAC 2222
 DB 2263 ATTTGAAGAGAAACAAAGAGAGCTGGAAGTGGAGAGACTGACAGACTCCAGAGAA 2322
 QY 2223 ACAGACCAAGCCCACTGAAGCTGTCTTAAAGTAACTACTCTTCCGCGTATGCG 2282
 DB 2323 GAAACCAACAGTATCTTACCTTTGGCTCATTTTGAAGTACAGATTCAGGGTCTATAC 2382
 QY 2283 AGTGAACAGATTTGGAGAGCTTGGCCAGCGAGGCTGTGAGACATTTTGAACGAAGC 2342
 DB 2383 CGTGAACGAATGAGGAGAGTCAAGCTTACAGCGCTGACAGCAATCATGAAACACACACC 2442

QY 2343 CTCAGAACAGATAAAAAACCCCAAGCTGTGAGAGAGCTGAGATCAGACTGATATTT 2402
 DB 2443 AGCAGCTCAAGATAGAAATCCAAACATTAAGGGTTCAAGCTCTCAACCCAGAGAAAT 2502
 QY 2403 GGAGATTAAGTGAAGCCCTTGAATGTTTGAATCTTAATGGCCAGGCTTCAAGTAA 2462
 DB 2503 GATTTAAAGTGGAGCTTTGAAATCCATGAGAGAGATGAGACAGGCTTGAAGTACAG 2562
 QY 2463 AGTTAGCTGCGCCAGAAAGATGATGATGAATGACATCTGTGTTGTGGCAATGT 2522
 DB 2563 AGTGAACCTGGAAGCCACAGGAGCCCACTGAGAGTGGAGAGAGAAAGAGTACAAAC- 2621
 QY 2523 ATCCAAATATATTTCTAGAGCAAGCCAACTTTGTCATACCTGATCAAAAGTTGAGC 2582
 DB 2622 --ACACATTTGGGGATGAGACCGCTGTCTATGCTCCCTTATGATGTCAGAGTCAAGC 2679
 QY 2583 CCTGAATGACATGGGGTTTGGCCCGGAGCCAGCTGTACATGAGCAATTCGAGAGAA 2642
 DB 2680 TATCAATCAATGAGATCTGGGCTGAGCCCTGACCTGATCAGTACTCTTATCTGAGAA 2739
 QY 2643 CCTCCCAATGCTGCTCTGGGAGAGTGTGATGATGATGATGATGATGATGATGATGAT 2702
 DB 2740 CTATCTGATACAGCTCCAGTATCATGAGGTTGAGAGCTTATTAACAGTATATGTTAA 2799
 QY 2703 GGTGACATGGAGCCAGTACTCTGAAAGCATCCGAGACACTTAAAGCTTATGAT 2762
 DB 2800 AGTTACTGTGTCAACAGTCTTCAAGAGACAGTACATGAGACGTGAAAGGCTATCAGAT 2859
 QY 2763 TTACTATGGAAGACCCAGATTCATTAAGAAACAGAGTGCATTTGAGAAAGAT 2822
 DB 2860 AAATGTTGAGAAACAAAGAGCTGTGAGATGAGAAACACATCCCAAGAGTGAACAT 2919
 QY 2823 CCTCACTTCCAGGACAGACACTCATGAGATGTTGCTGGGGCTAGAGCCCTTTAGCA 2882
 DB 2920 TCTAATGATTTTCAAGAACAAAGAACTGAGATGTTCTTCTTAATGCTTTAGTGA 2979
 QY 2883 CTACACACTGAATGTCCAGTGTGTCATGAGAGAGAGAGGAGCCAGCCCTGACAG 2942
 DB 2980 AATTCAATTAACAGTCTTACCTATTAATCTTAAAGAGCTGTGCTGAAAGTGAACCTTA 3039
 QY 2943 AGCTTTTAATATCCAGAGAGAGTCCAGTGTCTCCCTGCTTGAAGATTTGAATCC 3002
 DB 3040 TATATTTCAACACAGAGAGGATCTGAACAGCCAACTTTCTTAAGTCAATCAAGT 3099
 QY 3003 AACACTGACTCTTCACTTTGGAATGGATCAACCGAGCCACCCGAATGCAATTTGAC 3062
 DB 3100 TGAATGAAGACTGCACTTATCTTGGGAGTCACTTAAGAAATTAATGAAACTTAAC 3159
 QY 3063 AGAGTACACTTAAAGTATCAGCAATTAACAGACACATGAATTAAGGCTCTGTGAG 3122
 DB 3160 TGGCTATCTTTGCAATATCAATTAATTAATGACACTTACGAGATTTGGAATTAATGA 3219
 QY 3123 TTTGAAATTT---CTGCGCAACAGACCGTGAAGCTTTAAATTAATTTACAGAC 3179
 DB 3220 TATTAACATTAACATCAATCAAGCCAGCTGAGCCCTTCAACCTGAAATGCACTAC 3279
 QY 3180 TCGATATAGTTTATTTCTATGACAAACATCAAGAGATCAGAGATCAATTAACGA 3239
 DB 3280 CAAGTACAAATTTCTTCTGAGGCTTGAACCTTCAAGGCTGTGAAACCAATCAACGA 3339
 QY 3240 GGAA 3243
 DB 3340 GGAA 3343

RESULT 12
 US-10-435-751-164
 ; Sequence 164, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agnelys, Inc.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Chailite-Bid, Pia M.

/ APPLICANT: Jakobovits, Aya
 / APPLICANT: Raitano, Arthur B.
 / APPLICANT: Ge, Wangmao
 / TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 / TITLE OF INVENTION: Entitled 282Plg Useful in Treatment and Detection of Cancer
 / FILE REFERENCE: 51158-20084.00
 / CURRENT APPLICATION NUMBER: US/10/435,751
 / PRIOR FILING DATE: 2003-05-09
 / PRIOR APPLICATION NUMBER: 60/404,306
 / PRIOR FILING DATE: 2002-08-16
 / PRIOR APPLICATION NUMBER: 60/423,290
 / PRIOR FILING DATE: 2002-11-01
 / NUMBER OF SEQ ID NOS: 208
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 164
 / LENGTH: 7650
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-10-435-751-164

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
 Best Local Similarity 48.8%; Pred. No. 1.1e-127;
 Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

243 ACAGCCCTCCACATCACCACCAAGCTCTCCAAAGATTACATTATTGACCTCCGGAGAA 302
 367 ACGGTTCACATCATATAAAGCTCAAGTCCCAAGTGGCTTCCCTTGATGAGTA 426
 303 TATTTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTGAGCCGTA 362
 427 TTTTCAATTTGATGAGGCTAAAGGAATCCAGAACCAATTTCTGAGCTAAGA 486
 363 TGGGACTATTTTGATCATGATTAAGACCTCTGTCGACATGAGACCTGGACAGAA 422
 487 TGGCAACCTTTTATTATTCAGTCCATGATTAATTCATGACAAATTCAGAA---- 541
 423 GCTCAATTAATCATCATGAGGAGAAAGCTGAGACCTTAAGAGAGTCTATCAGT 482
 542 ----ACATTCAGATTCACAAAGAGGAGGACATATCTCTTCAAGGAATACCGCTG 597
 483 TACAGCAAGAAAGAAACCGGAGCTGCACTTTCTAATAACATTTGTCGCGCCATCCAG 542
 598 CTTTGCTTCAATAAATGAGGATGCTATGTCAGAAAGATTAATTAATGATTCAG 657
 543 ATCACCATTGTGACCAAGAAAGAACTTGAACCATCACTTCAAGTGTCACTTT 602
 658 TGTTCCTCAAACTCCCAAGAAAGAAATGACCTCTTGAAGTGAAGGAGATCCAT 717
 603 AGTACTCTCCCTGAGACCCCAATTGATTAACACCACTTAATTTTGGATGAGTA 662
 718 TGTCTCCCTCATCTCCCTCCCAAGGCTCCCACTTTTCAATTTATTTAGATGAT 777
 663 TTTCTTTCAAGACTTCCCAAGAGTGAAGTCTCAAGGTTTGAATGGGACCTTTA 722
 778 TGAATTTAGAACATCGAACAGATGAAGATTAATCATGAGCAAAAGGAGATCTATA 837
 723 TTTTTCCTAATGTCCTCCAGAGACACCGCGAAGATTAATCTGTTATGCTAATTA 782
 838 CTTTGGAAACGTGAAGAAAGAGACAGTGCATGCTACTGTGCTTGTGCTGCAATTTCC 897
 783 TCAATCTCAACCATACAGCAGAGCACTTATTTCTGAGAGGATTTCACTGAGTA 842
 898 AAGATTAGGACTATTTGTAAGAAATGCAATGAAATTAACATTAAGTTAAAGCA 957
 843 ATTGAATGACATTAATGCTTAATTTGAGTCACTGATTTTATGCTCAATTAAGCA 902
 958 TGTATATGACTCAAGTTATTCACAGAAATGTTTCAAGGCAATTCATCAAGCAAG 1017
 903 TGAAGAGAGCCCAACACTTTTAACTCAGAGGCAATGCAAGTAACAAAGAGAT 962
 1018 AAAACCCCAACTGCTGTTCCTCCCTGAGAGTGAAGTGAATCTTCAATTAACATCT 1077
 963 AAGAGAAATGCTTCACTGAGAGTGAATGCAAGAGAGTGCCTACCCCAATTAATTA 1022

1078 CAAGGGGAAATCTGCTGCTGAGTGTGTTGCTGAAGGCTTGGCCCACTCCACAGCTTGA 1137
 1023 CTGGCAAGAGAAATGTAATGCTAACCAAAAGAGCACTTTATTAAGACTTTAGAA 1082
 1138 TTGGAACAAATTTGTGTGTACTTAACAAAGGGAGAGAAACAAAGAAATTTAGGCA 1197
 1083 AACCTTGAGATCTATTCATGTTTTCAGAGCAGACTCTGAATTAACATGATTAAGCA 1142
 1198 GACTTTGAAGATAGAAATGCTCTTACAGAGCAAAAGAAATTAATCCCTCAGAGCAG 1257
 1143 AAATGATTAAGAGCATTCACCATTAATTTCTGTTAGATTAAGGCTCTCATCTG 1202
 1258 CAATTTCTTGGGAACAGCACTCAAGATTTTCACTTATTAAGAGAGCTCTCGCTG 1317
 1203 GATCAGACCTCTCAAAATCTTGTGCTCTCCCAAGAGAGATGAGACCTTGAATGCG 1262
 1318 GACAAAGAGCTCTGAGTGTGTATAGACCGGAAGCAATGCTATTTATATGTA 1377
 1263 AGCTAATGCAACCCCAACCAAGATTAAGCTGTTAACAATGAGTCCCAATGAAT 1322
 1378 GCTGAGAGAGACTTCAACCAATCAATGAGAGTCAATGCTCCCACTGAGTGA 1437
 1438 TCATCAATTTG---CTGATGATGTTGCTTCCCAAGGAATACAGTTTACCAACTTCA 1494
 1383 AGAAAGATCAAGTGAATATCAATGATGATGCTCTAATGAATTAATGATTTATGCTGC 1442
 1495 ACCAAATATATCTGCTGTATACAGTGTGAAGCTCAATATGCAATGATCTATCTTGC 1554
 1443 AAAGCATTTGAATGCTGCTGAGTGAAGCAACCAATGCTCACTGCAACACT 1502
 1555 CAATGCAATTTGATGTTGATGATGATGCTGCTCAATGATTAACAAAGATGAGAAA 1614
 1503 CTACAGGTCAATTCGAAACAGGCTGCTTTAATGATGATGCTCTTGTGCTCTCT 1562
 1615 TTAGCTACAGTGTGAGTGAAGTGTGCTTCTTCAATGATGAGTCTTGTGCTCACTGA 1674
 1563 CCCAATCATGAGTGTGTTAAAGAGCTTAAGAGAGTCTCTTCAATGAATTTATG 1622
 1675 GGCAGTCTGTCTGAGCAAGAGTGAAGAGTGAACCCCTGAGGAGGAGGATCA 1734
 1623 TTTTCAATGAATGAACTTTGAAATCAAGATGCTATGATGCTTAAAGAAATCC 1682
 1735 TATCATTAATTAATGCAATTCAGATCAAGAACCAAGAGATGCTGCTTTA 1794
 1683 TGTGCCCCAAGAGCACTACAGAACTTATACGTTGTTGCAAGAAATTAATGAGAT 1742
 1795 CTCAATGTTGGTGAAGAAATGCTATAGAAAGAACTGCAAGCAATTTGATTAAG 1854
 1743 GGCAGAAATGAAGTTCACTTACAGCCGAATATGCACTGTCGAAAGAGAGATG 1802
 1855 AAATGCTCAAAACTTAAGTTCCTCTTAAGAAATCTGTATCCCAATTTGCAATCT 1914
 1803 GTTCTTGAATGCAAGAGAAACATGATCAACCTTATCCCTCACTGCTGCTGCTGA 1862
 1915 TGAATTAATGTAAGCAAAATGACTCACTTTGAACACAGTTGAAGTGTCTG 1974
 1863 GGAACAACAGGAATCTGCTGATGTAAGAGTTCACTTTGACAGAGATCTATGATG 1922
 1975 GAGTAAATGAGAGAGCTTTGA-----AATTAATGCAAGAGATGAGAGAT 2025
 1923 AGCTAGTCAATGACATGACAGGAGCACTTACAGTGTGCTGCAACACACTGGA 1982
 2026 AATTAATGAGAGTAAATTTGACCAATCTTAATGTAATTTAAGGACCAAGATTTA 2085
 1983 CAGGCTCTCCGAGGCTGCTGTTAGCTGTTGCTCTTCACTCACTCAGCTCCGCT 2042
 2086 CTGCTTCACTCAATCTGCTTGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 2142
 2043 TTACATGCTCCCAATCTCTCTTTGACCTTGAAGATGACATCACTTGAACAAAGTGT 2102

Db 2143 TCTGTATGTCGCGATCCACAGAAAACCTTCACTTGTCTGAAGAAGACAGAGAGTGT 2202
Qy 2103 TCAGCTGTATGAGACCCGAGGCGATGACAACATATAGCCCATTTACAAAATTCATCATCGA 2162
Db 2203 TCGGCTGACCTGGGAAGCTGGAGCTGACACAAACAGCAATATTTAGGAGATATTTGTTGA 2262
Qy 2163 ATATGAGATGCAATGACAAAGCCAGGCTGTGGCAACCAAACTGAAGTTTCTGGAAAC 2222
Db 2263 ATTTGAAGGAACCAAAAGAGAGCTGGAGGTGGAGAACTGACAGAGTCCAAAGGAAA 2322
Qy 2223 AACAGCAACAGCCAGCTGAGCTGTCTCTTACGTAATCTCTTCCGGGTGATGGC 2282
Db 2323 GAAAAACCAAGTATCTTCACTTTGGCTCCATTTGGAGATACCACTTGAAGGTCTATAC 2382
Qy 2283 AGTGAACAGCATTTGGGAAGAGCTTGGCCAGGAGGCTGTGACAGTATTTGACGAAGC 2342
Db 2383 CGTGAACGAATGAGGAAGAGTCAAGCTTACGACCCGTACAGCATCATGAAACACACC 2442
Qy 2343 CTCAGAACAGATTAATAACCCCAAGCTGTGAAAGGATGGAATCAGAGCTGTATATTT 2402
Db 2443 AGCAGCTCAGATAGGAATCCAAATAAGGGTTCAAGCCTTCAACCCAAAGGAAT 2502
Qy 2403 GGAAGATTAAGTGAAGCCCTTGAATGTGTTCCATATTAATGGCCAGGCTTCACTACAA 2462
Db 2503 GATTATTAAGTGGAGCTTTGAAATCATGAGAGCAATGAGACCGCTTGAAGTACAG 2562
Qy 2463 AGTTAGCTGGCCGACAGAAAGATGTGATGATGAATGATCATCTGTGTGTGCAAAATGT 2522
Db 2563 AGTGAACCTGAAAGCCACAGAGAGCCCAATGAGTGGGAAGAAAGAAAGTCAAAACC- 2621
Qy 2523 ATCCAAATATATTTGTCTCAGGACCGCAACCTTTGTTCCATACCTGATCAAAAGTTACGC 2582
Db 2622 --ACACATTTGGGGTATGATGACGCTGTCTATGCTTATGATGTCAAGGTCCAGGC 2679
Qy 2583 CCTGAATGACATGGGGTTGGCCCGGACGACGTGATGATGAGGACATTTCTGGAGAAA 2642
Db 2680 TATCATATCACTAGAGATCTGGGCTGACCTCACTGACATCTCTATTTCTGGAGAAA 2739
Qy 2643 CCTCCCAATGTGGCTCTCTGGGAACGTGGTGAATGTGTGAACAGTACCTTAGCCGA 2702
Db 2740 CTATCTGTATACAGCTCCAGCTGATCATGGGGTGAACGTTTAAACAGTACATAGTTAA 2799
Qy 2703 GGTGACCTGGGACCCAGTACCTCTGAAAAGCATCCGAGACACTTCAAGGCTATGAT 2762
Db 2800 AGTATCTGTGTAACAGTTCCAAAGGACAGATGACATGACGCTGAAAGGCTATGAT 2859
Qy 2763 TTAATATTGGAAGACCCAGATTCATCTTAAAGAAACAGCTGACATTTGAGAAAAGT 2822
Db 2860 AATTTGGTGAAGAAACAAAAGCTCTGTGATGAGAAACATCCCAAGAAAGTGAACAT 2919
Qy 2823 CCTCACCTTCAAGGACGACAGCTCATGGCATGTTGCGGGCTGAGAGCCCTTAGCCA 2882
Db 2920 TCTAAGATTTTCAGGACAAAGAACTCTGSAATGTTCTTCTTGAATGCTTTTAGTGA 2979
Qy 2883 CTACACACTGAATGTCCGAGTGTCAATGGGAAAGGGGAGGCGCCAGCCCTTAGCAG 2942
Db 2980 ATTTCAATTAACAGCTTTAGCCATTAACCTTAAGAGAGCTGCTGAAAGTGAAGCTTA 3039
Qy 2943 AGCTTTAATTAATCCAGAAAGAGTCCCAAGTGTCTCCCTGTCTTTGAAGATTTGATATC 3002
Db 3040 TATATTTCAACACCGAAGAGATACCTGAAACAGCACTTTTCTTAAAGTCACTAAAGT 3099
Qy 3003 AACACGTGAGCTCTCACTTTGGAATGGGATCCAGGAGCCACCGAATGGGCTTTTGAAC 3062
Db 3100 TGAATAAGACAGCTCACTTTATCTTTGGGATCTACCTTAAGAAATTAATGGAACCTTAAC 3159
Qy 3063 AGAGTACACCTTAAGATACGCAATTAACAGACACATGATTAAGCCCTCTGTGTAGA 3122
Db 3160 TGGCTATCTTTTGCATATTCAGATTAATTAATGACACCTAGAGATTTGAGAAATTAATGA 3219
Qy 3123 TTTGAAATTT---CTTGCAACAGACAGGTGGACTTTTAAATAATTTAAATTTTCAAGC 3179
Db 3220 TATTAACATTAACAACTCCATCAAGGCCAGCTGGCACCTCTCAAACTCAATGCACTTAC 3279

Qy 3180 TCGATATAAGTTTATTTCTATGACAAACATCAGCAGATCAGAGCTCAAAATTTACGA 3239
Db 3280 CAAGTACAAATTTCTATGAGGGCTTGACATTTCAAGGAGCTGTGAAAACGATACCGGA 3339
Qy 3240 GGAA 3243
Db 3340 GGAA 3343

RESULT 13
US-10-435-751-170
; Sequence 170, Application US/10435751
; Publication No. US2004005348A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Paris, Mary
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Embodied 282PI3 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-20084.00
; CURRENT APPLICATION NUMBER: US/10/435,751
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 7650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-435-751-170

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
Best Local Similarity 48.8%; Pred. No. 1.1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

Qy 243 ACAGCTTCACCATCACTACCCCAACAGCTCTCCAAAGATTAATTAATGACCTCGGAGAA 302
Db 367 ACAGCTTCACCAATCATTAATAACAGTCAAAAGTCCAAAGTCCCTTCCCTGATGAGTA 426
Qy 303 TATTTAATTCAGTGTGAAGCCAAAGGAAACCCGCCAAGCTTTCTCTGACCCGTA 362
Db 427 TTTTCAAAATGATGTGAAGCTTAAAGAAATCCAGAACCAATTTGTGTGACTTAAGA 486
Qy 363 TGGGACTAATTTGACATGATAAGACCTCTGTGTCACATGAAGCTTGACAGAAC 422
Db 487 TGGCAACCTTTTATTTTACATGACCATCGATATTCATCATGAAACATTTGACGA----- 541
Qy 423 GCTCATTAATTAACATCATGAGGAGGAAAGAGTGAACCTATGAGAGATCTACAGT 482
Db 542 ----ACATTCAGAGATCCCAAGAGGAGGACATATCTCACTTTCAAGGAAATACCGCTG 597
Qy 483 TACACAGGAAGCAAGCCGAGCTGCAAGTTCTTAATAACATTTGTTCGCCCATTCAG 542
Db 598 CTTTCTTCAATTAACCTGGGAATGCTATGTGACAGAAATAGATTTATATGTTCCAG 657
Qy 543 ATCACCATTGTGAGCAAGAAATACTGAACCAATCACAATCTCAAGTGTGACGCTTT 602
Db 658 TGTTCCAAAACCTCCAAAGAAATAATGACCTCTTGAAGTGAAGGAGGAGATCCAAAT 717
Qy 603 AGTACTTCCCTGACAGACCCCAATTTGATTAACACACCACTTAATATTTTGTGATGATPA 662
Db 718 TGTCTCCCATGATCTCTCCCAAGGCTCCCACTTTACATTAACATTTATGATGAATAT 777
Qy 663 TTTCTTTCAAAAGCTTCCCAAAAGTGAAGTTTCTCAAGTTTGAATGGGAGACTTTA 722
Db 778 TGAATTAAGACATCGAAGCAAGATGAAGATATATATGAGCCAAAGGAGATCTATA 837

QY 723 TTTTCCAAATGTCCTCCAGAGACACCCGGAAGACTATATCTGTATCTAGATTAA 782
DB 838 CTTGGAACAGTGGAGAAAAGAGACAGTGGCAATGACTATGCTTGTCTCTCATTTCC 897
QY 783 TCACTACTCAAAACCAATACAGCAGAACCACTATTTCTGTAGAGTGAATTTCACTGATGA 842
DB 898 AAGATTAAAGCACTATTGTACAGAAAATGCCAAATGAAACTAAAGTTTAAAGCA 957
QY 843 ATTGAATGACATATAGCTGTAAATTTAGTGAACATGACTTTTATGCTCTAAATCAAG 902
DB 958 TGTCTAATGACTCAAGTTTATCAAGAAATTTGTTCCAAAGCAAAATTCATCAAGCAAG 1017
QY 903 TAGAGAGAGGCCCAACCAATTTTAACTCCAGAAAGCAATGCAAGTAAACAAGAGAAAT 962
DB 1018 AAAACCCAAATCTGCTGTGCTCCCACTGAGAGTGGCAGTACTTTCAATTAACATCT 1077
QY 963 AAGAGAAATGTGCTTCTCACTGAGTGCATTTGCAAGAAAGTCCCTAACCCCAATTAATTA 1022
DB 1078 CAAGGGGAAATCTTGTCTGTGAGTGTGCTGGAAGGCTTCCAACTCAAGGTGA 1137
QY 1023 CTGGGAAAGAAATGGAATGCTATCCCAAAAACAGACAGTTTATTAAGAACTTTGAGAA 1082
DB 1138 TTGGAACAAATTTGTGTGACTTACCAAGGGGAGAGAAACAAAAGAAATTTATGAGCA 1197
QY 1083 AACCTGCAGATCATTCATGTTTCAAGAGCACTCTGAAATTAACCAATGTATAGCAAA 1142
DB 1198 GACTTGAAAGATGAGAAATGTCTCTACAGAGCAAAAGAAATTTATGCTGCACAGCCAG 1257
QY 1143 AAATGCAATTAGAGCCATCAACCATACATTTCTGTAGAGTTAAAGCCGCTCATATCTG 1202
DB 1258 CAATTTCTTGGGAAACAGCCACTCAGATTTTCAAGTTATAGTAAAGAGCTCTCGCTG 1317
QY 1203 GATCAAGCCCTTCAAAATCTTGTGCTGTCTCCAGAGAGAGATGGAACCTTGTATGAG 1262
DB 1318 GACAAAGAAAGCCCTCAAGAGTGTGTATAGCACCGAGAGCAATGGGATCTTGTATGTGA 1377
QY 1263 AGCTTAAGCAACCCCAACCCAGAAATTTAGCTGTTAAACAAATGAGTCCCAATAGAAAT 1322
DB 1378 GGTGTAAGAGAACTTCAACCCCAATCAATGAGTGAAGATCAATAGCTCCCACTTGAACA 1437
QY 1323 TGCCCTGATGAGCCCGAGCAAGAAAATAGATGCGATACCATTAATTTTTCAAATGTGA 1382
DB 1438 TATATCATTTG---CTGTGTATGTTGTCTTCCCAAGGAAATGATTTTACCAACTTGA 1494
QY 1383 AGAAAGATCAAGTGCAGTATATAGTGCATGCTCTTAATGAATATGATATTTACTGCG 1442
DB 1495 ACCCAATCACTAGCTGTGTACAGAGTGAAGCTCAAAATGTCATGAACTATCTCTGC 1554
QY 1443 AAAGCAATTTGAATGTGCTGCTGAGCAACCAAGAACTCTACACCTGCAAAACACT 1502
DB 1555 CAATGCCAATATTGATGTGTGTGATGTCCGTTCATTTGATACAAACCAAGATGAGAAAA 1614
QY 1503 CTACAGAGTCAATGCAACAGAGCTGCTTTACTAGACTGTGCTTCTTGTGGTCTCTCT 1562
DB 1615 TTACGCTACAGGTGTGGGTACAGTGTCTTTCAATGCGAGTTCTTTGCTTCACTTGA 1674
QY 1563 CCCAACATGAGTGTTTAAAGAGCTAAAGAGTGTCTTTCATGAAGATATTTATGT 1622
DB 1675 GGCAGTGTGTCTCTGCAAGAGTGAAGAAAGTAAACCTGGAAGGCGAGGATATA 1734
QY 1623 TTTTACATGAATGAACCTTTGAAATCAAAAGATGCTATAGATGCTTAAAGAAATTC 1682
DB 1735 TATCTATGAAATGAGCAATGCAATGCAACAGAACACCGAAAGATGCTGGCTTGA 1794
QY 1683 TGTGGCCCAAAAGACAGTACAGAACTTATACGTGTGTGCAAGGATTAATTTAGGAT 1742
DB 1795 CTCATGTTGGTGAAGAAATGCTATAGAAATACTGCAAGCCAAATTTGGATTTAG 1854
QY 1743 GGCAGAAATGAATTCATACAGCCGAAATATGCAATTTGCAAGAGGAGAGATGT 1802
DB 1855 AAATGCTACAAACTTAGAGTTTCTCTTAAGAACTCTGTAATCCCAAAATTCATATGCT 1914

QY 1803 GTTCCTTGAATGCAAGTGAAGAAACATGATCAACCTTATCCCTCACTGTCTGTGCTGAA 1862
DB 1915 TGAATTTACATTTGAAAGCAAAATGTGATCTCAATTTTGAACAAGTTTGAAGTTGTCTG 1974
QY 1863 GGAACAAGAGAACTGCCCCAGTGAAGAAAGTTCACTGTTGACAGAGATCATTAATGTGT 1922
DB 1975 GAGTAAAGATGAGAAAGCCCTTTGA-----AATTAATGACAGAAAGATGAGAGAT 2025
QY 1923 AGCTGATGTCAGTGAACATGACAGGCGGAGCTTACAGTGTGTGGCCCAACACACTGTGA 1982
DB 2026 AATTTATGATGAGCTAATTTGACATATCTAATGTATCTTAAGAGACCAAGTATTTTA 2085
QY 1983 CAGGCTCTCCGAGCGCTGTCTTACAGCTGTGTCTCTTACTCCAACTCCAGCTCCGT 2042
DB 2086 CTGCTGTACGCTCACTGCTCTGAGAGTGTGCGGAT---TAACTCAAGTATCTGT 2142
QY 2043 TTAAGATGCCAAATCTCTCTTTGACTTAAGATCAATCAACCTTGAACAAAATGT 2102
DB 2143 TCTTGATGTTCCGAGATCCACAGAAAACCTTCACTGTCTGAAGACAGAAAGAGTGT 2202
QY 2103 TGAGCTGTACAGACCCCGAGGATGACAAATAGCCCATTAACAAATTCATCATGCA 2162
DB 2203 TCGGCTGACCTGGAGAGCTGAGCTGACCAACAGCAATATTTAGAGATATTTGTTGA 2262
QY 2163 ATATGAAGATGCAATGCAACAGCCAGGCTGTGCAACCAACCTGAAGTTTCTGGAAC 2222
DB 2263 ATTTGAAGAAACAAAGAAAGCTGTGAAGTGTGGAAGAACTGACAGAGTCCAGAGAA 2322
QY 2223 ACAGACCAAGCCAGCTGAAGCTGTCTTACGTGAACATACCTCTTCCGCTGTATG 2282
DB 2323 GAAACCAAGTATCTTACTTTGCTTCAATTTGTGAGATATACAGTTCAAGGTCTATAC 2382
QY 2283 AGTGAACAGCATTTGGAAGAGCTTCCAGCAAGCGCTGTGCAAGTATTTGACAAAG 2342
DB 2383 CGTGAACGAAGTGAAGAGTCACTGACCGCTGACACATCAATGAAGAACACACAC 2442
QY 2343 CTCAAGAACAGATTAACAAACCCCAAGCTGTGAAGAACTGAGATCAAGACCTGATATTT 2402
DB 2443 AGCACTCTCAAGTATGAAATTCACAAACATTAAGGTTCAAGCTTCAACCCAAAGAAAT 2502
QY 2403 GGAAGATTAAGTGAAGCCCTTGAATGTGTTGAAATCTAATGAGCCAGGCTTCAATCA 2462
DB 2503 GATTAATAAGTGGAGCTTTGAAATTCATGAGACAGATGAGCAAGGCTTGAAGTACAG 2562
QY 2463 AGTACCTGTGGCCCAAGAAAGATGTGATGATGAATGACATCTGTGTGTGSCAAATGT 2522
DB 2563 AGTGAACCTGGAAGCAACAGGAGCCCAAGTGAAGTGAAGAAAGAAACAGTCAAAACC- 2621
QY 2523 ATCCAAATATATTTGTCTCAGGACGCCCAACCTTGTCCATCTGATCAAAAGTTCAAGC 2582
DB 2622 --ACACATTTGGGGTGAATGAGCCCTGTGTCTATGCCCTTATGATGTCAAGGTCCAGGC 2679
QY 2583 CCTGATGACATGAGGTTTGGCCCGAGCCAGCTGTAGTCAATGAGCAATTCGAGAGAA 2642
DB 2680 TATCAATCAATGAGATCTGGGCTGAGCCCTGACCTCAAGTCACTCTAATTCGAGAGAA 2739
QY 2643 CTTCCCAATGTGTCTCTGAGAAAGTGTGTGAATGTGTGAACAGTACTTGAACCGCA 2702
DB 2740 CTATCTGATACAGCTCAGTGTATCATGTGGGTGACCTTATTAACAGTATCAATTTGTTAA 2799
QY 2703 GGTGACCTGGAGCCAGTACCTGTGAAGAAAGATCCGAGAGCAACCTTAAGAGGTATCGAT 2762
DB 2800 AGTTACTGTGTACAGATTTCCAAAGACAGAGTACATGAGCTGTGAAGAGGCTATCAAGT 2859
QY 2763 TTAATATTGAAGACCAAGATTCATCTTAAGAAACAGAGTCACTATGAGAAAGAT 2822
DB 2860 AAATTTGTGAGAAACAAAGATCTGTGTGAAGAGAAACATCTCCAAAGAGTGAACAT 2919
QY 2823 CTTACCTTCCAGGACAGACATGATGATGTGCGGGGCTGAGAGCCCTTTAGGCA 2882
DB 2920 TCTAAGATTTTCCAGGACAAAGAACTGTGAATGTGTTCTTCAATGATGCTTTTATGGA 2979
QY 2883 CTACACACTGAATGTCCGAGTGTCAATGTGGAAGAGGAGCCAGCCAGCCCTGACAG 2942

Db 2980 ATTTCATTAAACAGCTCTTAGACCTATATACCTTAAAGAGCGTCTGAAAGTAGCCTTA 3039
 QY 2943 AGCTTTTATATATCCGAAAGAGATCCCGAGTGTCTCCCTGCTTTGAAGATTGTGATCC 3002
 Db 3040 TATATTTCACAAACCCAGAAAGAGTACTGAAACAGCACTTTTCTAAAGGTATCAAAAGT 3099
 QY 3003 AACACTGACCTCTCTCACTTTTGGATGGATCCAGGAGCCACCAATGGCATTTTGGAC 3062
 Db 3100 TGATTAAGACACGCGCACTTATCTTGGGAGCTAAGTAATTAATTAATTAATTAATTAAT 3159
 QY 3063 AGAGTACACCTTAAAGTATGAGCAATTAACAGCAGACATGAATTAAGCCCTCTGTGTA 3122
 Db 3160 TGCGCTATCTTTTSCATATATCAATTAATTAATGACACCTAGAGATTGAGAAATTAATGA 3219
 QY 3123 TTTGAAATTT---CTGCGCAACAGACAGGTGGACTTTAAATTAATTTGAGAC 3179
 Db 3220 TATTAACATTACAACTCCATCAAAAGCCAGCTGGCACTCTCAACCTGAATGCACTAC 3279
 QY 3180 TCGATTAAGTTTATTTCTATGACAAACATCAGAGATCAGAAATCAATTTACAGA 3239
 Db 3280 CAAGTCAAAATTTCTACTTGAAGGCTTGCACTTACAGGGCTGTGAAAAACCATCAAGCA 3339
 QY 3240 GGAA 3243
 Db 3340 GGAA 3343

RESULT 14

US-10-435-751-176
 ; Sequence 176, Application US/10435751
 ; Publication No. US2004005348A1
 GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; TITLE OF INVENTION: Entitled 282P13 Useful in Treatment and Detection of Cancer
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT APPLICATION NUMBER: US/10/435,751
 ; PRIOR FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 176
 ; LENGTH: 7650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-435-751-176

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
 Best Local Similarity 48.8%; Pred. No. 1.1e-127;
 Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

QY 243 ACAGCCTCCAAACATCAACCAAGTCTCCAAAGATTACATATTATGACCTCGGGAGAA 302
 Db 367 ACAGGTTCCAAACATCAATAAAGTCCAAAGTCCAAAGTCTTCCCTTGATAGTA 426
 QY 303 TATTTATTCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTGACCCGTAA 362
 Db 427 TTTTAAATTTGATGTGAAGCTAAAGGAATCCAGAACCAATTTTGGGACTAAGG 486
 QY 363 TGGGACTCATTTTGAATGATTAAGACCTCTGTGTCACCATGAAGCTGGCAGAGAAAC 422
 Db 487 TGGCAACCCCTTTTATTTCACTGACCATGGATTAATTCATGAAACATTCAGGA----- 541
 QY 423 GCTCAATTAATTAACATATATGAGGAAGGAAGTGAAGTATGAAGAGTATATGATG 482

Db 542 ----ACATTACAGATCCCAACAGAGGGGACATATCTCACTTTCAAGGAAATACCGCTG 597
 QY 483 TACAGCAGGAACGAAACCGGAGCTGACGTTTCTAATAACATGTTGTCGCCCATCCAG 542
 Db 598 CTTTCTTCAATTAATCTGGGAATGTCTATGTCAAGAAATAGATTTATATGTTCCAG 657
 QY 543 ATCACCATTGTGGAACCAAGAAATCTTGAACCATCACTCAAGTGTGACTCTTT 602
 Db 658 TGTTCACAAACCTCCAAAGAAATTTGACCTCTTGAAGTGAAGGAGATCCAT 717
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 Db 718 TGTCTCCATGCAATCTCCCAAGGCTCCCACTTTAACAATTATTTGATTAATAT 777
 QY 663 TTTCTTGAAGACTTCCAAAGGAGAGAGTTTCTAAGTTTGAATGGGAGCTTTA 722
 Db 778 TGAATTTGAACATGAAACAAAGATGAAGATATATAGAGCCAAAGGAGATCTATA 837
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 QY 843 ATTGAATGACATATATGCTGCTAATTTGATGACACTGATGTTTATGCTCAATATCAG 902
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 QY 903 TAGAGAGAGGCGACCAACATTTTAACTCCAGAAAGCATGCAATTAACAAAGAGAAAT 962
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 Db 1318 GACAAAGAGCCTCAGAGTGTGTATAGACACCGGAGCAATGGCATTTGTATATGGA 1377
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 QY 1323 TGCCTGTATGACCCCGAGAGAAATATAGATGGCATACATTTTTCAAATGTTCA 1382
 Db 1438 TCATCATTTG---CTGTGATGTTGTCTTCCCGAGGAAATCAAGTTTATCAACCTTCA 1494
 QY 1383 AAAAAATCAAGTCAATATATCAATGCAATGCTCTAATGAATATGATATTTATCTGGC 1442
 Db 1495 ACCAATATCACTGCTGTGTACAGTGTGAAGCTCAATATGTCATGGAATCTATCTTGC 1554
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 Db 1555 CAATCCAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614
 QY 1503 CTACAGGCTATTTGAAACAGGCTGCTTTAAGTACTGATGCTTCTTTGGTCTCTCT 1562

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
 Best Local Similarity 48.8%; Pred. No. 1,1e-127;
 Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

QY	243	ACAGCTCCAAACCATCAACCAAGTCTCCAAAAGTTACATTATTGACCTCCGGAGAA	302
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QY	303	TATGTAACTCACTGGAAGCCAAAGGAAACGCCCCCAAGTTTCCGTGACCCGTAA	362
DB	427	TTTTCAATTAATGAAAGTAAAGGAAATCCAGAACCAATTTTCGTGACCTAAGAA	486
QY	363	TGGAGTCAATTTGACATCATGAAGACCTCTGTCACCATGAAGCTGACAGAAAC	422
DB	487	TGGCAACCTTTTATTTTACCTGACATGGATTAATTCATGAAACAATTACAGA	541
QY	423	GCTCATTAATTAATCATCATGAGGAGGAAAGCTGAGACCTTAAGAGAGTCTATGATG	482
DB	542	---ACATTCAGAGTCCCAACGAGGGGACATATCTCACTTTCAGAGGAAATACCGCTG	597
QY	483	TACAGAGGAAAGAAACGAGAGCTGACAGTTTCTAATTAATTTGTTGTCGCCATCCAG	542
DB	598	CTTGTCTTCAATAAATCTGGGAATCGCTATGTAGAAAGAAATGAATTAATGTTCCAG	657
QY	543	ATCACCATTTGTGAGCCAAAGAAAACCTGAAACCAATCACACTTCAAGTGTGATCTTT	602
DB	658	TGTTCCAAAATCTCCAAAGAAAATTAATGACCTCTTGAAGTGAAGAGAGATCCAT	717
QY	603	AGTACTTCCCTGAGACCCCAATTTGATTAACCACTAATAATTTTGAATGATGA	662
DB	718	TGTCTCCATGCAATCTCCCAAGGCTCCACCTTTTACATTTATTTGATGAATAT	777
QY	663	TTCCTTTCAAGACTTCCAAAGTGAAGAGTTTCTCAAGTTTGAATGGGACCTTTA	722
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QY	783	TCTACTCAAAACATACAGAGAGCAACTATTTCTGTAAGGTGATTTCACTGATGA	842
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DB	1018	AAAACCAAACTGCTGTGCTCCCACTGAGATGAGTGTCTTCAATTAACATCTCT	1077
QY	963	AAGAGAAATGCTCTTCACTGAGTGTGATGCAAGAGACCTGCTCAACCAATTAATTTA	1022
DB	1078	CAAAAGGGGAAATCTTGCTGCTTGAAGTGTGCTGAAAGGCTTGCCAACTCAAGGTGA	1137
QY	1023	CTGGGCAAGAGATGGAATGCTAACCAAAACAGACAGTTTAAAGAACTTTGAA	1082
DB	1138	TTGGAACAAAATTTGTGTGATCTTACCAAAAGGAGAGAAACAAAAGAAATTAATGCA	1197
QY	1083	AACCTTGACATCATTTTTCAGAAAGACACTGTGAAATTAACAAATGTTATACAA	1142
DB	1198	GACTTTGAAGATGAAGATGTCTCTACAGAGCAAAAGAAATTAATGCTGACACCGAG	1257
QY	1143	AAATGATTAAGAGCCATCCACATATCAATTTCTGTTAAGGTTAAAGCGGCTCATATG	1202
DB	1258	CAATTTCTTGGGAAAGCCACTACGATTTTCACTTATATGTAAGAGAGCTCTCGCTG	1317
QY	1203	GATCAAGAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGAGATGGACCTTAATCTGAG	1262
DB	1318	GACAAAGAAAGCTCAGAGTGTGTATATGACCCGGAAGCAATGGATCTTGTATATGTA	1377

QY	1263	AGCTAATGCAACCCCAACCCAGAAATAGCTGTTAAACAATGAGTCCCAATAGAAAT	1322
DB	1378	GGCTAAGAGAACTCAACCCCAACATCAATGAGAGTCAATGGCTCCCAAGTTGACAA	1437
QY	1323	TGCCCTGATGACCCACAGCAAAAAATGATGCGATACATTAATTTTTTCAATGTTCA	1382
DB	1438	TCATCCATTTG---CTGTGATGTGTCTTCCCAAGGAAATCACTTTTACCAACTTCA	1494
QY	1383	AGAAAGATCAATGACATATATCACTGCAATGCTCTAATGAATATGATATTTTCTGGC	1442
DB	1495	ACCAATATATCTGCTGTGTACAGTGTGAAGCTCAATGTCCATGGAATATCTCTTGC	1554
QY	1443	AAAGCAATTTGTAATGTGCTGCTGAGCCACCAAGAAATCTCACACTGCAACACACT	1502
DB	1555	CAATGCCAATATTTGATGTTGTGAGATGCTGCTCATTTGATTAACAAACAAAGATGAGAA	1614
QY	1503	CTACAGATCATTTGAAACAGGCGCTTTACTGACGTGCTCTTGGGTGCTCT	1562
DB	1615	TTAGCTACAGTGTGGGTACAGTCTTTCTTACATTTGCAAGTCTTTGCTTACCTGA	1674
QY	1563	CCCAACCATCGAGTGTTTAAAGAGCTAAAGAAAGTCTCTTCAATGAAGATATTATGT	1622
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QY	1623	TTTACATGAATAATGGAATTTGGAATCAAGATGCTAATGATGTTTAAAGAAATTC	1682
DB	1735	TATCTATGAATAATGCAATTTGCAATGATCAACGAACCAACGAAGATGCTGGGTCTTA	1794
QY	1683	TGTGCCCCAAAGGACATGACAGAACTTAATGCTGTGTTGCAAGAAATTAATGGAAT	1742
DB	1795	CTCATGTTGGGTAGAAATGCTATGAGAAACATGCAATCAAGCAATTTGATATTAG	1854
QY	1743	GGCAAGATGAAATGTTCACTTACAGCCCAATATGCAATGTCGCAAGAGGAGATGAT	1802
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QY	1803	GTCCTTTGAATGCAAGTGAACATGATCAACCTTATCTCTGCTGCTGCTGAA	1862
DB	1915	TGAATTAATCTGTGAACCAAAATGTGACATCATTTGAAACAGATTTGAAGTTCTCTG	1974
QY	1863	GGACAAAGAGAACTGCCAGTATGAAGATGTCCTGTTGACAGATCATATGATGT	1922
DB	1975	GAGTAAAGATGAGAGGCTTTGA-----AATTAATGACAGAAAGATGAGAGAT	2025
QY	1923	AGCTGATGCACTGACATGACAGAGGAGCACTACAGTGTGAGCAACACACTCTGGA	1982
DB	2026	AATTAATGATGAGCTAATTTGACATATCTAATGTAATCTTTAGAGACCAAGATTTTA	2085
QY	1983	CAGGCTTCCGCAAGCTGTGCTTGAAGCTGTGCTCTCACTCAACTCCAGCTCCGT	2042
DB	2086	CTGCTGTTCAAGCTCATTAAGCTCTAGACAGTGTGCTCCGATA---TAACTCAAGTAACTGT	2142
QY	2043	TTACGATGCTCCAAATCTCTCTTTGACTTGAATCACTGACAGATCACTTGAACAAAGGT	2102
DB	2143	TCTTAATGTTCCGATGACCAAGAAACCTTCACTGTGCTGAAAGACGAAGAGAGGT	2202
QY	2103	TCAGCTGATGAGACCCAGAGGATGACAAATATGCCCCCATTAACAAATTCATCATGA	2162
DB	2203	TGGGCTGACCTGGAAGCTGAGCTGACCAACAGCAATATTAACGATATATTTGTA	2262
QY	2163	ATATGAAGATGCAATGCAACAGCCAGGCTGTGGAACAACAACTGAAGTTTCTGGAAC	2222
DB	2263	ATTTAAGGAACAAAGAAAGGCTGGAAGGTGGAAGAACTGACCAAGATTCAGAGAAA	2322
QY	2223	ACAGACCAAGCCAGCTGAAGCTGTCTCTTAAGTGAATTAATCTCTTCCGCTGATGGC	2282
DB	2323	GAAAACCAAGTATCTTAACCTTTGCTTCATTTGTGATTAACAGTTTCAAGGCTATAGC	2382
QY	2283	AGTGAACGATTTGGAAGAGGCTCCCAAGAGGCTGTGAGAGTATTTTGAACAAAGC	2342
DB	2383	CGTGAACGAATGAGGAAGATGAGCTTGAAGCCAGCCGCTAGACCATATGAACACCAAC	2442
QY	2343	CTCAGAACCATATAAAACCCCAAGCTGTGGAAGGACTGGGATCAAGACCTGATTAATTT	2402

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 21:48:06 ; Search time 9787 Seconds
(without alignments)
12613.697 Million cell updates/sec

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Perfect score: 4134
Sequence: 1 cttcaagctcccgcatga.....cggtagagagatatttc 4134

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: em_esthum:*
3: em_estlin:*
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5: em_estcov:*
6: em_estdpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_dln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
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24: em_gss_pro:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2265.4	54.8	4178	11	AK087693 Mus muscu
2	647.8	15.7	2394	11	AK045259 Mus muscu
3	632.2	15.3	788	14	CF737289 UI-M-HD0-
4	631.8	15.3	639	9	AL134791 DKFZp547K

5	628.8	15.2	3166	11	AK048567 Mus muscu
6	625.6	15.1	639	14	CB294617 12B22031
7	615.4	14.9	806	13	B0615094 UI-M-FR0-
8	603.6	14.6	794	14	CF533313 UI-M-FR0-
9	602.4	14.6	757	13	B0612550 UI-M-FR0-
10	601.4	14.5	824	14	CA327466 UI-M-FR0-
11	598.8	14.5	752	14	CF741342 UI-M-GH0-
12	598.8	14.5	3037	11	AK052440 Mus muscu
13	580.4	14.0	753	14	CA316157 UI-M-FW0-
14	553	13.4	594	13	BX505499 DKFZp661
15	551.8	13.3	775	14	CD804797 UI-M-GH0-
16	549.6	13.3	800	9	AU130055 UI-M-GH0-
17	548	13.3	998	13	B0715777 AGENCOURT
18	545.4	13.2	943	13	B0505113 AGENCOURT
19	544.4	13.2	726	14	CF737303 UI-M-HD0-
20	536.6	13.0	962	13	B0504945 AGENCOURT
21	531.2	12.8	769	14	CB313432 AGENCOURT
22	531	12.8	826	13	B0604950 AGENCOURT
23	528.2	12.8	670	14	CF173249 B0920F06-
24	526	12.7	782	13	B0446008 UI-M-EU1-
25	519.2	12.6	733	12	B1739003 603359825
26	515.8	12.5	609	10	BE257386 601109220
27	509	12.3	754	14	CB289933 UI-M-FR0-
28	508.8	12.3	644	14	CB518611 UI-M-GH0-
29	502.2	12.1	732	14	CB249525 UI-M-EX0-
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33	483	11.7	722	14	CB519500 UI-M-GH0-
34	482	11.7	737	14	CF533329 UI-M-FR0-
35	465.8	11.3	623	13	B0308392 MRO-BT450
36	465.4	11.3	697	14	CF534203 UI-M-FR0-
37	464.2	11.2	904	12	B1756933 603029138
38	463.2	11.2	696	14	CB527865 UI-M-FR0-
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41	452	10.9	1586	11	AK039322 Mus muscu
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45	439	10.6	4919	11	BC040674 Homo sapi

ALIGNMENTS

RESULT 1
AK087693
LOCUS
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN
full-length enriched library, clone:R330007H08 product:NRCA
PROTEIN homolog (Homo sapiens), full insert sequence.
ACCESSION AK087693
VERSION AK087693.1 GI:26104446
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency, full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
AUTHORS
TITLE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE 20493374
PUBMED 11042159

REFERENCE
AUTHORS
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Matsubara, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
20530913
11076861

TITLE
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE
JOURNAL
REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS
6
(bases 1 to 4178)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hamagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S.,
Takekida, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Yamamoto, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
Location/Qualifiers

FEATURES
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/clone_stage="2 days pregnant adult"
1. 4178
/note="NRCAM PROTEIN homolog (Homo sapiens) (SPTK10.5179,
evidence: FASTA, 95.3%ID, 18*length, match=705)"

ORIGIN
Query Match 54.8%; Score 2265.4; DB 11; Length 4178;
Best Local Similarity 83.1%; Pred. No. 0;

Matches 2743; Conservative 0; Mismatches 396; Indels 160; Gaps 8;
QY 1 CTTCAAGTCCCGCCATG-AAATTACTTAACGTTACACACCAAGTTCCAGAAATCT 59
DB 391 CTTCAAGTCCCGCCATGAAAAATTTTAAAGCCGACAC-----CAATCT 439
QY 60 TTTGTAAGAAAGAAAGAAATTCAGTGTGAGTCTCAGCAGAGTTAAGTAATCA 119
DB 440 TCCGTAAGAAAGAAAGAAATTCGTCGGGTCTCAGCAGAGTGCAGCTGATCA 499
QY 120 GCTTAATTAATCCGAAAGAAAGCGTTATTCGCGGCGAGAGTCCGATCTCTT 179
DB 500 GCTTAATTAATCCGAAAGAAAGCGTTATTCGCAAGCGAGTCCGATCTCTT 559
QY 180 CCGTGCAGATGATTAAGTCACTGAGTACCTTGTATCCAAACTTCTGAAGACTT 239
DB 560 CCGTGCAGATGATTAAGTCACTGAGTACCTTGTATCCAAACTTCTGATC-----T 601
QY 240 GGTACAGCTCCCAACATCAACCAAGTCTCCAAAGATTAATTAATTAACCTCGGA 299
DB 602 GGTACAGCTCCCAACATCAACCAAGTCTCCAAAGATTAATTAATTAACCTCGGA 661
QY 300 GAATTTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTGACCG 359
DB 662 GAATTTGTAATCCAGTGTGAAGCCAAAGGAAACCTCCCAAGCTTTCTGACCTG 721
QY 360 TAATGGAATCTATTTGATGATTAAGAAACCTTGTGATCAATGAAGCTGACAG 419
DB 722 TAATGGAATCTATTTGATGATTAAGAAACCTTGTGATCAATGAAGCTGACAG 781
QY 420 AACGCTCAATTAATCAATGAGGAAAGGAAAGCTGAGACTTGAAGAGTCTATCA 479
DB 782 AACCTTGCATCAATCAATGAGGAAAGGAAAGCTGAGACTTGAAGAGTCTATCA 841
QY 480 GGTACAGGAAAGGAAAGGAGGAGGAGTCTTGAATTAATGATGTCGCGCATC 539
DB 842 GGTACAGGAAAGGAAAGGAGGAGGAGTCTTGAATTAATGATGTCGCGCATC 901
QY 540 CAGATCACCATTGTGAGCAACCAAGAAAGAACTTAACCAATCACTTCAAGTGTGATC 599
DB 902 TTAGGATCCTTGTGAGCAACCAAGAAAGAACTTAACCAATCACTTCAAGTGTGATC 961
QY 600 TTTAGTACTTCCCTGAGACCCCAATGATTAACCAACCACTTAATTTGATGAG 659
DB 962 ATTAGTACTTCCCTGAGACCCCAATGATTAACCAACCACTTAATTTGATGAG 1021
QY 660 TAATCTCTTCAAAAGCTTCCAAAGTGAAGAGTCTTCAAGTGTGATGAGGACT 719
DB 1022 TAATCTCTTCAAAAGCTTCCAAAGTGAAGAGTCTTCAAGTGTGATGAGGACT 1081
QY 720 TTAATTTTCAATGTCCTCCAGAGACACCGCGAAGACTATATCTGTTAGTAGATT 779
DB 1082 TTAATTTTCAATGTCCTCCAGAGACACCGCGAAGACTATATCTGTTAGTAGATT 1141
QY 780 TAATCATCTCAAAACATTAACAGAGAGCAACCTATTTCTGAAAGTGAATTCAGTGA 839
DB 1142 TAATCATCTCAAAACATTAACAGAGAGCAACCTATTTCTGAAAGTGAATTCAGTGA 1201
QY 840 TGAATTTGAATGACATTAATGCTGCTAATTTGAAGTGAAGTGAATTTGATGATC 899
DB 1202 TGAATTTGAATGACATTAATGCTGCTAATTTGAAGTGAAGTGAATTTGATGATC 1261
QY 900 AAGTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 959
DB 1262 AAGTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321
QY 960 ATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019
DB 1322 ATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1381
QY 1020 TTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1079
DB 1382 TTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1441

Qy	1080	AAAAACCTTGAGATCATTCATGTTTGAAGAGACGCTGGAATTACCATGATATAGC	1139
Db	1442	GAAAACTGTGAGATCACTCATGTTTCCGAAGCCACCTGTGAATTATATCGATGATGC	1501
Qy	1140	AAAAAATCATTTAGGAGCGCATCCACCATACCATTTCTGTAGAGTTAAAGGGCTCCATA	1199
Db	1502	AAAAAACCCATTAGAGAGCCGTCCATCACCATTTCTGTACTGTAAAGGGCTCCCTA	1561
Qy	1200	CTGATACAGACCCCTCAAAATCTTTGTGCTGTCCCAAGAGAGATGGGACTTGTATCTG	1259
Db	1562	CTGATGCTGTGCACTCAAAACCTGTCTTTCCCGGGAGAGATGGGACCTCATCTGTG	1621
Qy	1260	CAGAGCTATATGGCAACCCCAAAACCGAATTAGCTGTAACTAATATGATGCCAATAGA	1319
Db	1622	CAGAGCTATATGGCAACCCGAATTTAGCTGTAACTAATATGATGCCAATAGA	1681
Qy	1320	AATTGCCCTCATGTAGCCCCAGAGAAAATATGATGGCGATACCATATATTTTCAAAATGT	1379
Db	1682	AATTGCTTGCATGACCCCAAGAAAATATGATGGCGATACCATATATTTTCAAAATGT	1741
Qy	1380	TCAAGAAAGATCAAGTGCATATATCACTGCAATGCCCTATATGATATATGATATTTACT	1439
Db	1742	TCAAGAAAGCTCAAGTGGGTTTATCACTGCAATGCCCTATATGATATATGATATTTACT	1801
Qy	1440	GGCAAAAGCATTTTGTAAATGTGTGCTGTAGCGCACCAAGAAATCCTCACACTCGAAACAC	1499
Db	1802	AGCAAAATGCATTTGTAAATGTGTCTGTAGAACCAACTGTGAAATTCATCATCAGCAAAACAC	1861
Qy	1500	ACTCAACAGGTCATGTGCAAAAGGCCGTCTTATGACATGTGCTCTTTGGGTCTCC	1559
Db	1862	ACTCAACAGGTCATGTGCAAAAGGCCGTCTTGTCAATGTGTGCTCTTTGGATCTCC	1921
Qy	1560	TCTCCCAACCATTCGAGTGGTTTAAAGAGCATAAAGGAAGTCTCTTACATGAAGATATTTA	1619
Db	1922	TATGCTCATACATTTAGTGTGTTTAAAGGACATAAGGAAGGCCCTCTTACATGAAGACATTTA	1981
Qy	1620	TGTTTTACATGAAAAATGGAACTTTGGAAATCAAAAGATGCTACATGATCGTTAAAGAAAT	1679
Db	1982	TGTTTTGCATGATATATGGAACTTT-----AGAAAT	2011
Qy	1680	TCTGTGTGGCCCAAAAGGACAGTACAGGAATTATACGTGTGTGTGCAAGAAATTAATTAGG	1739
Db	2012	TCCGTGTGGCCCAAAAGGATAGTATGACAGGACGTATATCTGTGTGTGCAAGAAATTAATTAGG	2071
Qy	1740	GATGGCAAAAGATGAAGTTCACTT-----ACAGCC	1769
Db	2072	GATGGCAAAAGATGAAGTTCACTTGGAAATCAAAAGATGCAACAGAGATCATTAACAAC	2131
Qy	1770	CGAATATGCACTGTGTGCAAAAGAGGAGCATGTGTCTTTGATATGCAAAATGAAACATAGA	1829
Db	2132	TGAGTATGCACTGTGTGCAAAAGAGGAGCATGTGTCTTTGATATGCAAAATGAAACATAGA	2191
Qy	1830	TCACACCTTATTCCTCACTGTCTGTGTGTGCTGAAGGACAAAGGAACTGCCAGTATGA	1889
Db	2192	CCACACCTTATTCCTCACTTATGTGTGTGTGCTGAAGGACAAAGGAACTGCCAGTATGA	2251
Qy	1890	AAGGTGTCATGTGTGCAAAAGATCATCTATAGTGTGTGTGCTGATGCTGATGACATATGACAGCG	1949
Db	2252	AAGGTGTCATGCTGCACTGCAAAAGATCATCTGTGTGTGTGTGCTGATGCTGATGACATATGACAGCG	2311
Qy	1950	GACCTACACGTGTGTGCGCAACCAACTCTGTGACAGCGTCTGCCACAGCGCTGTGCTTAG	2009
Db	2312	AACCTACACGTGTGTGCGCAACCAAGCTGTGACAGCGTCTGCCACAGCGCTGTGCTTAG	2371
Qy	2010	CGTTGTGTGCTCTTACTCCAACTCAGCTCCGTTTACGATGTCCCAATCTCTCCCTTTGA	2069
Db	2372	GGTTGT-----CGATGTCCCGAATCTCTCCCTTTGA	2401
Qy	2070	CTTGAAGATGACATGCAATCTGCAAAAGTGTCACTGTGTCATATGAGACCCAGAGCGATAGA	2129
Db	2402	TTTGAAGATGACATGCAATCTTGTGCAAAAGTGTGTCACTGTGTCATATGAGACCCAGAGCGATAGA	2461

OY	2130	CAACAATAGCCCCCTTACAAAATTCATCATGGAATATGAATATGCAATGACACACAGG	2189
Db	2462	CAACAATAGCCCCCTTACAAA-----G	2487
OY	2190	GCTGTGGCACCACCAAACTGAAGTTCTTGAAACAACAACAAGCCC-AGCTGAAGCTGT	2241
Db	2483	GCTGTGGCGCCACCAAGGCTGAAGTTCTTGAAACAACAACAAGCCCAGGCTGAAGCTGT	2544
OY	2249	CTCCTTACGTGAACCTACTCTTCCGCGTGATGAGCAATGAACAAGCATTTGGAAAGCTTGC	2306
Db	2543	CTCCCTATGTGACACTACTCTTCCGCTGCATGAGAAACAAGCATTTGGGAAAGTATGC	2602
OY	2309	CCAGCGAGGCGCTGAGCAGTATTTGAACGAAGCCTCAAGACCAATTAACCCCAACG	2366
Db	2603	CGAGCGAGGCGCTCGAGCAGTATCTTAACGAAGCCGAAGACCAAGATCAAAATCCACAGG	2666
OY	2369	CTGTGGAAGAAGCTGGGATCAGAGCCGTGATTAATTTGSAAGTTACGTGAAGCCCTTGAATG	2422
Db	2663	CTGTGGAAGAAGCTAGGAGCAGAGCCGGAACAATTGTGATTAACATGGAAGCCCTGGAATG	2722
OY	2429	GTTTCGAATCTAATGGGCGCAGGCGCTTCAGTACAAAGTTAAGTGGCGCGCAGAAAGTGTG	2488
Db	2723	GTTTTCATCAATAGGGGCTGGGCTGCCAGTCAAAAGTAGCTGGGCGCAGAAAGATGTGTG	2782
OY	2489	ATGATGATGAGACATCTGTGTTGTGTGGCAATGTATCCAAATATATTTCTCAGGACAGC	2544
Db	2783	ACGATGATGAGACCTCTGTGTGTGTGGCAATGTATCCAAATATCAATGTCTCTGGCACAC	2844
OY	2549	CAACCTTGTGTCACCTATCACTGATCAAAGTTACAGGCGCTGATAGCACTGGGAGTTTGCCCG	2606
Db	2843	CAACCTTGTGTCACCTATCACTGATTAAGTTCAAGCTCTGATGATGTGGGGTTTGACACAG	2906
OY	2609	AGCCAGCTGTAGTATGAGGACATTCTGGAGAAGACCTTCCAAATGTGGCTCTTGGAAACG	2666
Db	2903	AGCCAGCTGTAGTATGAGGAGCATTTCTGGAGAAGACCTTCCAAATGTGGCTCTTGGAAATG	2966
OY	2669	TGCGTGTGAATGTGTGTGAACAATCTTAGCCGAGGTGACCTGGGACCCAGTACTCTGCA	2722
Db	2963	TTCCGCTGAGGTGTGTGAACAATACGCTGTGGAGGTGACCTGTGGAACCCAGTCTCTCCCA	3022
OY	2729	AAAGCATTCGAGGACACCTTACAAAGGCTATGGGATTTACTATTGGAAAGCCAGAGTTCAT	2788
Db	3023	AGAGTGTCCGAGGACACTTACAAAGGCTATCGGATTTACTCTGGAAGACCCAGAGCTCTT	3088
OY	2789	CTAAAGAAACAGACGTTCACATTGAGAAAAGATCTTCACCTTCCAGAGCAGCAAGCTC	2844
Db	3083	CTAAAGAAACAGAGCGCCACATTGAGAAAGATCTTCACCTTCCAGAGCAGCAAGACTC	3144
OY	2849	ATGCGATGTGTCGGGGGCTAGAGCCCTTTAGCCACTACACACTGAATGTCCGAGTGTCA	2906
Db	3143	ACGGCATGTGTCAGGGGCTGAGGCATTAACGTACTAATGACCTTCAACGTCGAGAGTGTCA	3202
OY	2909	ATGGGAAAGGGAGAGGCGCCAGCCAGCCCTGACAAAGTCTTAAATATCTCAAGAGAGTCC	2966
Db	3203	ACGGGAAAGGGAGAGGCGCCAGCCAGCCAGCAAGAGGCTTCAATACACCGAGAGGAGTCC	3266
OY	2969	CCAGTGTCCCTCGTCTTTGGAAGATTGGAATTCACAACCTGAGCTCTCTCACTTTGGAAT	3022
Db	3263	CTAGTGTCCCTCACTCTTTGGAAGATTGGAATTCACAACCTGAGCTCTCTCACTTTGGAAT	3322
OY	3029	GGGATTCACCGAGCACCCGAGATGCAATTTTGAACAGATACACCTTAAGTATGAGCCAA	3088
Db	3323	GGGACCCCCCAGGCAACCCAAATGTGCAATCTGACTGATGATCATCTTAACATATGAGCCAA	3388
OY	3089	TTAAACAGACACATGAAATTAGGCCCTCTGTGTAGATTGAAAATTCCTGCCAAACAAGAC	3148
Db	3383	TTAAACAGACACATGAACTAGGCCCTCTGTGTAGATTTAAAAATTCCTGCCAAACAAGACC	3442
OY	3149	GGTGAAGCTTTAAATAATTTAAATTTGACACTGCATATTAAGTTTATTTCTATGACACAA	3208
Db	3443	GCTGGAAGCTTTGAAAATTTAAATTTGACACTGCATATTAAGTTTCTATTTCTATGACACGA	3502
OY	3209	CATGAGCAGATCGAAGTCAAAATTTACAGAGAAGCAGTAAACAATGTGATGAAGCT	3267

QY 475 TATCAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 534
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 Db 586 TACAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 645
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 QY 535 CCATCCAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 594
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 Db 646 CCATCCAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 705
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 QY 595 CAGTCTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 654
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 Db 706 CAGTCTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 765
 |||||
 QY 655 ATGAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 714
 |||||
 Db 766 ATGAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 825
 |||||
 QY 715 GACCTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 774
 |||||
 Db 826 GACCTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 885
 |||||
 QY 775 AGATTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 834
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 Db 886 AGATTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 945
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 QY 835 GTGAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 894
 |||||
 Db 946 GTGAGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1005
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 QY 895 AATCA 900
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 Db 1006 GAGTTA 1011

RESULT 3
 CF737289 788 bp mRNA linear EST 10-OCT-2003
 LOCUS UI-M-HDO-ckr-1-15-0-UI-r1 NIH_BMAP_HDO Mus musculus cDNA clone
 DEFINITION IMAGE:30610358.5', mRNA sequence.
 CF737289
 ACCESSION CF737289.1 GI:37633625
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 788)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaab@r-mail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyx-5.
 Location/Qualifiers
 1..788
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30610358"
 /isue_type="whole eye"
 /dev_stage="embryo 12.5,13.5,14.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP HDO"
 /note="Organ: Eye; Vector: pyx-Asc; Site_1: EcoR I;"

Site 2: Not I; The library was constructed according
 Bonaudo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TTAATGAGT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH).

Query Match 15.3%; Score 632.2; DB 14; Length 788;
 Best Local Similarity 88.2%; Pred. No. 1.9e-164;
 Matches 696; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

QY 833 CAGTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 892
 |||||
 Db 1 CAGTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 60
 |||||
 QY 893 CTAAATCAAGTGTACAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 952
 |||||
 Db 61 CTAAATCAAGTGTACAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 120
 |||||
 QY 953 AAGAGCAATTAAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1012
 |||||
 Db 121 AAGAGCAATTAAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 180
 |||||
 QY 1013 CAATATTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1072
 |||||
 Db 181 CAATATTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 240
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 QY 1073 ACTTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1132
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 Db 241 ACTTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 300
 |||||
 QY 1133 GTATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1192
 |||||
 Db 301 GTATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 360
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 QY 1193 CTCATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1252
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 Db 361 CTCATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 420
 |||||
 QY 1253 TGATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1312
 |||||
 Db 421 TGATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 480
 |||||
 QY 1313 CAATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1372
 |||||
 Db 481 CAATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 540
 |||||
 QY 1373 CAATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1432
 |||||
 Db 541 CAATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 600
 |||||
 QY 1433 ATTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1492
 |||||
 Db 601 ATTTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 659
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 QY 1493 CAATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1552
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 Db 659 CAATGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 719
 |||||
 QY 1553 GGTGTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1612
 |||||
 Db 720 GGTGTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 779
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 QY 1613 ATATTGTGTACAGCAAGCAAGCAAGCGAGCTGACGTTTCTATATACATGTTGTCGCC 1671
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Db 780 ACATTATG 788

RESULT 4
AL134791 639 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZP547K0690.r1.547 (synonym: hfbp1) Homo sapiens cDNA clone
DEFINITION DKFZP547K0690.5, mRNA sequence.
ACCESSION AL134791
KEYWORDS
VERSION AL134791.1 GI:6602978
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 639)
Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and
Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 91 sequence available.
This clone (DKFZP547K0690) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..639
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP547K0690"
/issue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="547 (synonym: hfbp1)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

ORIGIN

Query Match 15.3%; Score 631.8; DB 9; Length 639;
Best Local Similarity 99.5%; Pred. No. 2.2e-164;
Matches 633; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1013 CAATTATTACGGGGAAGGAAGATGCTACCCAAAAACAGACAGTTTATTAAGA 1072
|||||
1 CAATTATTACTGGGGAAGGAAGATGCTACCCAAAAACAGACAGTTTATTAAGA 60
|||||
1073 ACTTTGAGAAAACCTTGAGATCATGTTTCAGAGCAGACTGTGAAATTACCAAT 1132
|||||
61 ACTTTGAGAAAACCTTGAGATCATGTTTCAGAGCAGACTGTGAAATTACCAAT 120
|||||
1133 GTATAGCAAAAAATGCAATTAGAGCAGATCCACATTCATTGTTAAGTTAAAGCG 1192
|||||
121 GTATAGCAAAAAATGCAATTAGAGCAGATCCACATTCATTGTTAAGTTAAAGCG 180
|||||
1193 CTCACATGCGATGACAGAGCCCTCAAAATCTGTGTCGCCAGAGAGATGGAGCT 1252
|||||
181 CTCACATGCGATGACAGAGCCCTCAAAATCTGTGTCGCCAGAGAGATGGAGCT 240
|||||
1253 TGATCTGACAGAGCTAATGGCAACCCCAAAACCAAGATTAGCTGTAAACAAATGAGCTC 1312
|||||
241 TGATCTGACAGAGCTAATGGCAACCCCAAAACCAAGATTAGCTGTAAACAAATGAGCTC 300
|||||
1313 CAATAGAAATGGCCCTGATGATGACCCAGAGAAAAATAGATGGCGATACATTATTTT 1372
|||||
301 CAATAGAAATGGCCCTGATGATGACCCAGAGAAAAATAGATGGCGATACATTATTTT 360

Qy 1373 CAATGTTCAAGAAAGATCAAGTCAGTATATCAATGCAATGCCCTATATGAAATGAGAT 1432
|||||
Db 361 CAATGTTCAAGAAAGATCAAGTCAGTATATCAATGCAATGCCCTATATGAAATGAGAT 420
|||||
Qy 1433 ATTTACTGGCAAAAGCAGATTTTAAATGTCGCTGAGACCCACAGCAATCTCTACACCTG 1492
|||||
Db 421 ATTTACTGGCAAAAGCAGATTTTAAATGTCGCTGAGACCCACAGCAATCTCTACACCTG 480
|||||
Qy 1493 CAACACAGCTTACAGAGTCATGCAACAGAGCCCTGTTTACTAGACTGTGCTCTCTTG 1552
|||||
Db 481 CAACACAGCTTACAGAGTCATGCAACAGAGCCCTGTTTACTAGACTGTGCTCTCTTG 540
|||||
Qy 1553 GGTCTCTCTCCCAACATGAGTGTAAAGAGAGCTAAAGAAAGTCTCTTCAATGAAG 1612
|||||
Db 541 GGTCTCTCTCCCAACATGAGTGTAAAGAGAGCTAAAGAAAGTCTCTTCAATGAAG 600
|||||
Qy 1613 ATATTATGTTTATCATGAAATGGAACCTTGGAAA 1648
|||||
Db 601 ATATTATGTTTATCATGAAATGGAACCTTGGAAA 636
|||||

RESULT 5
AK048567 3166 bp mRNA linear HTC 20-SEP-2003
LOCUS AK048567
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:G130076007 product:NRCAM PROTEIN homolog [Homo
sapiens], full insert sequence.
ACCESSION AK048567.1 GI:26339411
VERSION AK048567.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS
TITLE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20499374
MEDLINE 11042159
PUBMED
REFERENCE
AUTHORS
TITLE
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, Y.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL 20530913
MEDLINE 11076861
PUBMED
REFERENCE
AUTHORS
TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
JOURNAL
REFERENCE
AUTHORS
TITLE
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL

REFERENCE 6 (bases 1 to 3166)
 AUTHORS Aduchi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Komori,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.
 URL:http://genome.gsc.riken.go.jp/
 URL:http://fantom.gsc.riken.go.jp/.
 Location/Qualifiers

FEATURES
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ORIGIN
 Query Match 15.2%; Score 628.8; DB 11; Length 3166;
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 Matches 685; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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RESULT 6
 CB294617 639 bp mRNA linear EST 28-FEB-2003
 LOCUS 12B22031 rev.1 F02_r_027.ab1 Chimpanzee brain library Kooos Pan
 DEFINITION troglodytes cDNA clone 12B22031 rev.1_F02_r_027.ab1 5' similar to human NRCAM Bravo, mRNA sequence.

ACCESSION CB294617
 VERSION CB294617.1 GI:28620047
 KEYWORDS EST.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 Hellmann,I., Zollner,S., Bhard,W., Eberberger,I., Nickel,B. and Paabo,S.
 Selection on human genes as revealed by comparisons to chimpanzee cDNA

TITLE JOURNAL
 COMMENT Genome Res. (2003) In press
 CONTACT: Paabo S
 Max-Planck-Institute for evolutionary Anthropology
 Deutscher Platz 6, 04103 Leipzig, Germany
 Tel: +49-(0)-341-3550 500
 Fax: +49-(0)-341-3550 555
 Email: paabo@eva.mpg.de
 Seq primer: M13 reverse.
 Location/Qualifiers

FEATURES
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/notes="Vector: pUC19, Site 1: SfiI-A, Site 2: SfiI-B; The library was prepared using the SMART cDNA library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid vector."

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ORIGIN

Query Match 15.1%; Score 625.6; DB 14; Length 639;
 Best Local Similarity 99.1%; Pred. No. 1.2e-162;
 Matches 628; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 66 CCAAACTGAAGTTCTGGAACACAGACAGCCGAGCTGAGCTGTCTTACGTGA 125
QY 2262 CTACTCTCTCCGCGTGTGAGTGAACAGCATTTGGAAAGCTTCCAGAGGCGTC 2321
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DB 246 GGGATCAGAGCCGATTAATTTGGAGATTAGTGAAGCCCTTGAATGTTTGAATCTGA 305
QY 2442 TGGGCGAGGCTTCACTACAAAGTTAGTGGCGCCAGAAAGATGTGATGATGATGAC 2501
DB 306 TGGGCGAGGCTTCACTACAAAGTTAGTGGCGCCAGAAAGATGTGATGATGATGAC 365
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RESULT 7
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 LOCUS BU615094
 DEFINITION UI-M-FRO-cbe-f-02-0-UI.r1 NIH BMAP_FRO Mus musculus cDNA clone
 ACCESSION BU615094
 VERSION BU615094.1 GI:23281321

KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia; Eutheria; Chordata; Sciuromorphi; Muridae; Murinae; Mus.
 1 (bases 1 to 806)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
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 location/Qualifiers
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 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 14.9%; Score 615.4; DB 13; Length 806;
 Best Local Similarity 85.9%; Pred. No. 9.5e-160;
 Matches 693; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

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QY 2168 AAGATGCAATGACAAAGCGAGGCTGTGGACCAACAAATGAAATTTCTGGAACAGCA 2227
DB 61 AAGATGCAATGACAAAGCGAGGCTGTGGACCAACAAATGAAATTTCTGGAACAGCA 120
QY 2228 CCACAGCCGAGTGAAGCTGTCTCTTACGTAATCTCTTCCGCGTGTGAGTGA 2287
DB 121 CCACAGCCGAGTGAAGCTGTCTCTTACGTAATCTCTTCCGCGTGTGAGTGA 180
QY 2288 AAGCATTTGGGAAAGCTTTGCCAGGAGGCTCTGAGCATGATTTGACGAAGCTCAG 2347
DB 181 AAGCATTTGGGAAAGCTTTGCCAGGAGGCTCTGAGCATGATTTGACGAAGCTCAG 240
QY 2348 AACCATTAATAACCCAGAGCTGTGGAAGCATGGATTCAGAGCTGATTAATTGAGAGA 2407
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QY 1618 TATGTTTACATGA 1632
 Db 780 TTTCATGATATGA 794

RESULT 9
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 VERSION BU612550.1 GI:23278765
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC <http://imgc.nci.nih.gov/>.
 1 (bases 1 to 757)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

Location/Qualifiers
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FEATURES
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/lab_host="PH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP F10"
/note="Organ: Brain; Vector: pYX-Asc; Site: 1: Ecor I; Site: 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP), supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 14.5%; Score 601.4; DB 14; Length 824;
Best Local Similarity 87.1%; Pred. No. 7.7e-156;
Matches 659; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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295 CGGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354
307 CGGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
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415 AAGAGAACTCTATTAATCATCATGAGCGAAGGAAAGCTGAGACCTATGAGAGTCT 474
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487 TACCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
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595 CAGTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
607 CAGTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
655 AAGGATTAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 714

Db 667 ATGATTAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
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727 GACCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
775 AGATTTAATCACTCAACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
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RESULT 11
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DEFINITION UT-M-GH0-cl1-k-18-0-UT-r1 NIH_BMAP_GH0 Mus musculus cDNA clone
IMAGE:30618401 5', mRNA sequence.
CF741342
CF741342.1 GI:37637680
EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
source

Location/Qualifiers
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30618401"
/tissue_type="whole brain"
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/lab_host="PH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX-Asc; Site: 1: Ecor I; Site: 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP), supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 14.5%; Score 598.8; DB 14; Length 752;
Best Local Similarity 87.9%; Pred. No. 3.9e-155;
Matches 662; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

878 CTGAGTTTATGAGTCTAATCAAGTAGAGAGCGCAACATTTTAACTCCAGAG 937

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Db	60	GCAATGAAGAAGCCACAAGAGGAATTAGAGGAAACGTGCTTTCCCTGAGTGCATTGCGG	119
Qy	998	AAGGACGTGCCATACCCCATTTATTAATCTGGGGAAGAGGAATGGAAATGCTACCCAAAAACA	1057
Db	120	AAGGCTTACCTACCTCAATTTATTTATCTGATATCAAGAAAGAGGAATGCTTCCGCGCACC	179
Qy	1058	GGACAGTTTATTAAGAACTTTGAGAAAACCTTGACAGATCATTTTCATGTTTCAGAAACAGACT	1117
Db	180	GGACATTTTATTCGAACTTTTAAGAAAACCTTGACAGATCATCATGTTTTCGAAACCGACCT	239
Qy	1118	CTGGAATTTACCAATGTATAGCAAAAAATGCAATTAGAGCCATCCATCCATTCTGT	1177
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Qy	1478	GAATCTGACACCTGCAAAACACACTCTAACAGTCAATGGCTGCAAAACAGGCTGCTTTACTAG	1537
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DEFINITION	Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone: D430023606 product: NEUROSPASIN (FRAGMENT) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK052440		
VERSION	AK052440.1	GI:26095186	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	1 Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		

TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20493574
PUBMED	11042159
REFERENCE	
AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoh, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M., Sumi, N., Itoh, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, K., Ozawa, K., Tanaka, T., Matsunuma, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1-to 3037)
AUTHORS	Aachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirose, T., Horii, F., Imctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoh, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001)
REFERENCE	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genomics-res@gsc.riken.go.jp).
COMMENT	URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216
FEATURES	cDNA library was prepared and sequenced in Mouse Genome Encyclopædia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
misc_feature	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ location/Qualifiers
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ORIGIN

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Query Match 14.5%; Score 598.8; DB 11; Length 3037;
Best Local Similarity 54.0%; Pred. No. 7.9e-155;
Matches 1371; Conservative 0; Mismatches 1092; Indels 77; Gaps 4;

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RESULT 13
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 CA316157
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CA316157 753 bp mRNA linear EST 09-JUL-2003
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 IMAGE:6812372 5', mRNA sequence.
 CA316157
 CA316157.1 GI:24534281
 EST.
 Mus musculus (house mouse)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 753)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: DYX-5.
 Location/Qualifiers
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FEATURES
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/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACG. This library was created for the University, Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

[illegible]

RESULT 14
 LOCUS BX505499 594 bp mRNA linear EST 04-SRP-2003
 DEFINITION DKFZp686i17202.r1.686 (synonym: hicc3) Homo sapiens cDNA clone
 ACCESSION BX505499
 VERSION BX505499.1 GI:32034972
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 594)
 Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
 Mewes, H.W., Well, B., Amid, C., Osanger, A., Fodor, G., Han, M. and
 Wiemann, S.
 EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,
 Wellenreuther, R., et al.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No si sequence available.
 This clone (DKFZp686i17202) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubneweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /note="Vector: pT7.1; Site_1: SfiI; Site_2: SfiI;
 cDNA-collection"

ORIGIN
 Query Match 13.4%; Score 553; DB 13; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.1e-142;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2749 CAAGCTTATCGATTACTTATGGAAGCCAGAGTCTTCTTAAAGAAACAGAGCTCAG 2808
 |||||
 DB 1 CAAGCTTATCGATTACTTATGGAAGCCAGAGTCTTCTTAAAGAAACAGAGCTCAG 60
 QY 2809 ATTGAGAAAAGATCTTCACTTCCAAAGGACCAAGATCATGTCGTCGGGGCTA 2868
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 DB 61 ATTGAGAAAAGATCTTCACTTCCAAAGGACCAAGATCATGTCGTCGGGGCTA 120
 QY 2869 GAGCCCTTTAGCCACTACACTGATGTCCAGTGTGTCATGGAAGGAGGAGGCGCCA 2928
 |||||
 DB 121 GAGCCCTTTAGCCACTACACTGATGTCCAGTGTGTCATGGAAGGAGGAGGCGCCA 180
 QY 2929 GCGAGCCCTTGAGAGAGTCTTAAATCTCGAAGAGAGTCCCAAGTCTCCCTGCTTTTG 2988
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 DB 181 GCGAGCCCTTGAGAGAGTCTTAAATCTCGAAGAGAGTCCCAAGTCTCCCTGCTTTTG 240
 QY 2989 AAGATTGTAATTCACAACCTGAGCTCTCACTTTGGAATGGATTCACAGGACCCG 3048
 |||||
 DB 241 AAGATTGTAATTCACAACCTGAGCTCTCACTTTGGAATGGATTCACAGGACCCG 300
 QY 3049 AATGCAATTTTACAGAGATGACCTTAAAGTATCAGCCAAATTACAGCACATGATTA 3108
 |||||
 DB 301 AATGCAATTTTACAGAGATGACCTTAAAGTATCAGCCAAATTACAGCACATGATTA 360

QY 3109 GGCCTCTGTAGATTGTAATTCCTGCAACAAGACGCTGACCTTTAAATTTA 3168
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 DB 361 GGCCTCTGTAGATTGTAATTCCTGCAACAAGACGCTGACCTTTAAATTTA 420
 QY 3169 AATTTCAGCACTCGATATTAAGTTTATTTCTATGCAACAACATCAGAGATCAGAGT 3228
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 DB 421 AATTTCAGCACTCGATATTAAGTTTATTTCTATGCAACAACATCAGAGATCAGAGT 480
 QY 3229 CAATTACAGAGAGCACTACCACTGTGATGTAAGCTGTATCTTCCACTATGTA 3288
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 DB 481 CAATTACAGAGAGCACTACCACTGTGATGTAAGCTGTATCTTCCACTATGTA 540
 QY 3289 GGTGACGCAAG 3301
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 DB 541 GGTGACGCAAG 553

RESULT 15
 LOCUS CD804797 775 bp mRNA linear EST 15-JUL-2003
 DEFINITION UT-M-GW0-cig-m-20-0-UT.1 NIH_BMAP_GW0 Mus musculus cDNA clone
 ACCESSION CD804797
 VERSION CD804797.1 GI:32463623
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 775)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: PYX-5.

FEATURES
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 Site 2: Not I; The library was constructed according
 to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into PYX-Acc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CTGGCTCTG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemmi Chan, Ph.D.,
 program coordinator."

ORIGIN

